

Fig. 1

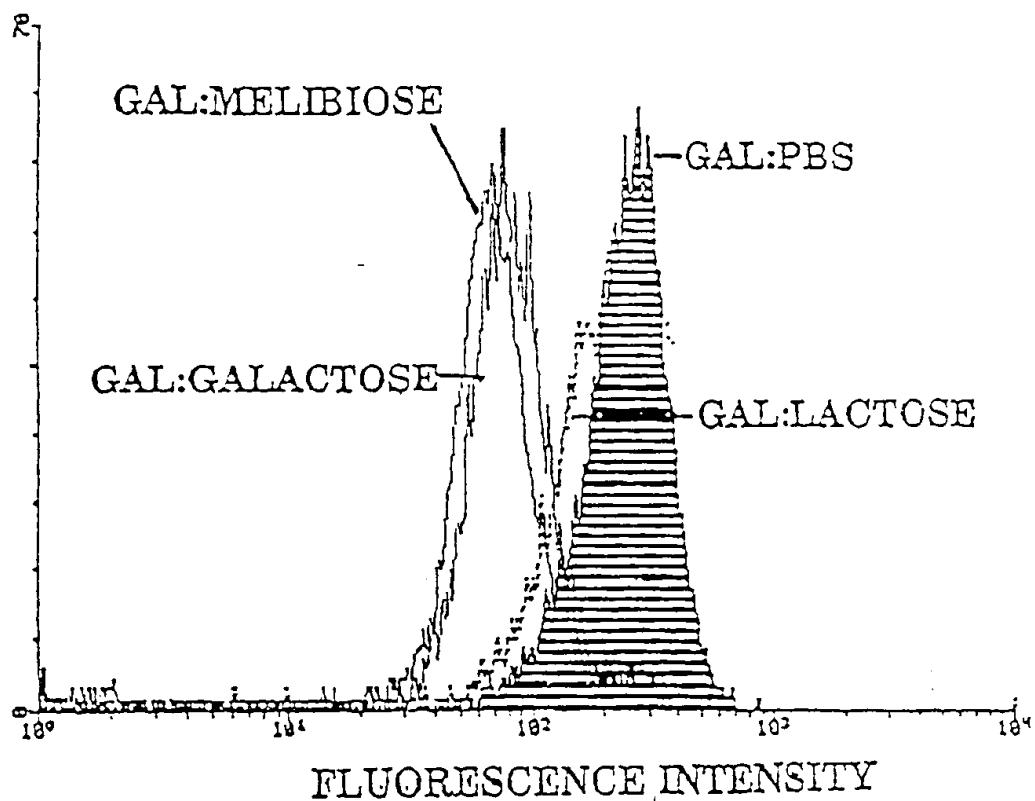


FIGURE 2

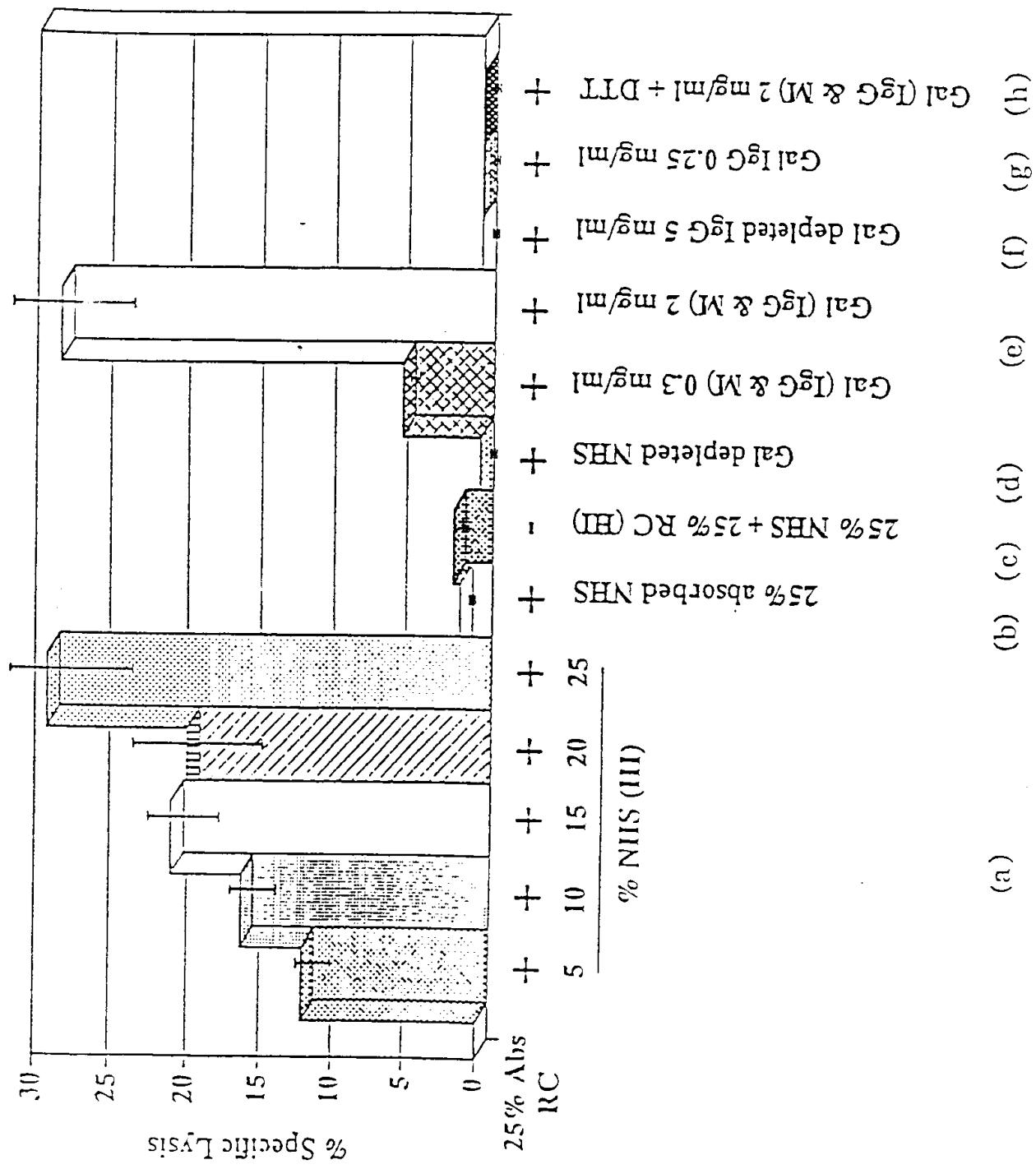
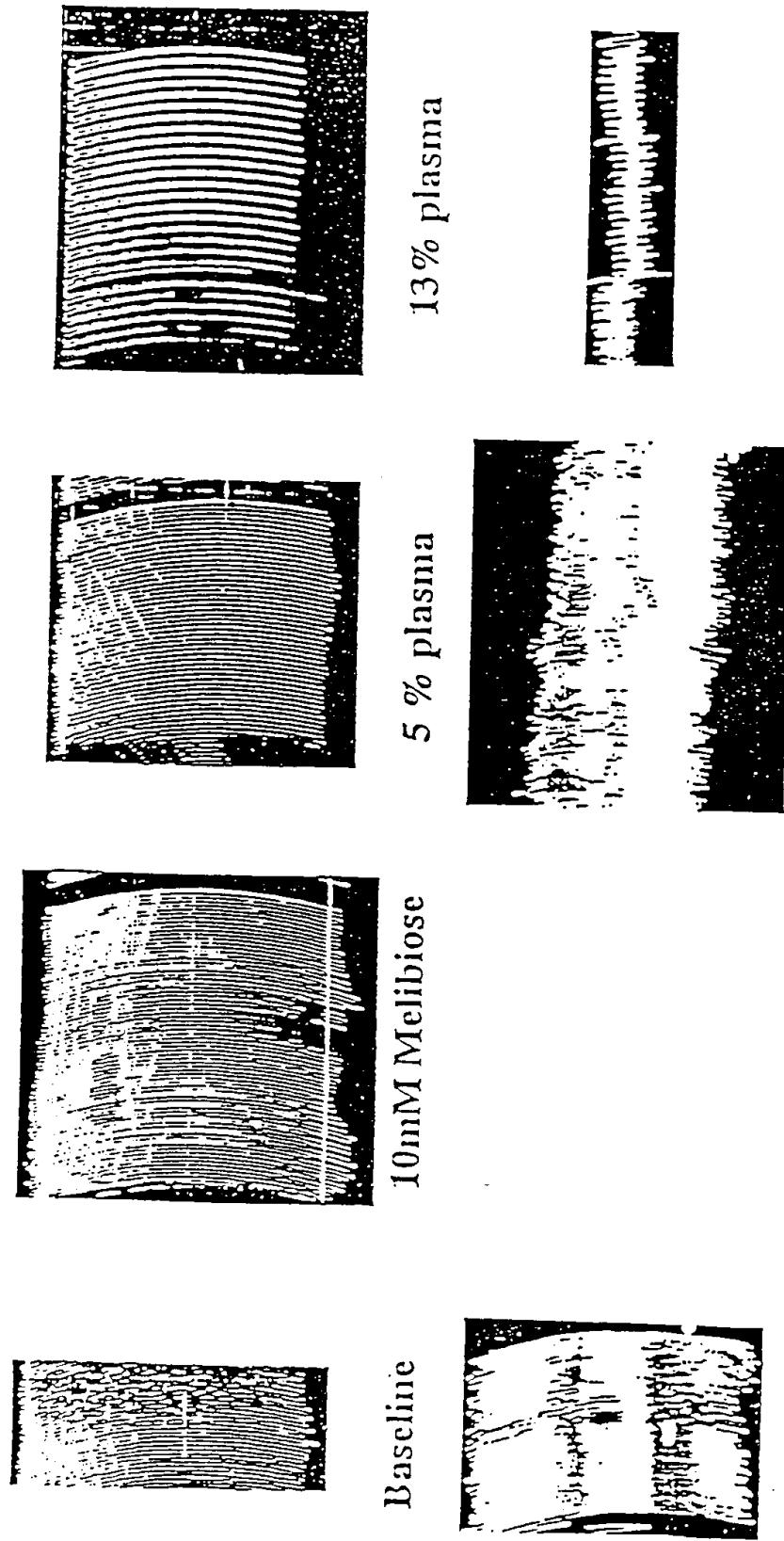


FIGURE 3



F5  
DNA Blotting (Int):

PCTC9	1	-----	-----	-----	50
BOVGSTA	1	cccccccccc	cccccccccc	cccccccccc	50
MUSGLYTN8	1	-----	-----	-----	50
PCTC9	51	-----	-----	-----	100
BOVGSTA	51	cccccccccc	cccccccccc	cccccccccc	100
MUSGLYTN8	51	-----	-----	-----	100
PCTC9	101	-----	-----	-----	150
BOVGSTA	101	cccccccccc	cccccccccc	cccccccccc	150
MUSGLYTN8	101	-----	-----	-----	150
PCTC9	151	-----	-----	-----	200
BOVGSTA	151	cccccccccc	cccccccccc	cccccccccc	200
MUSGLYTN8	151	-----	-----	-----	200
PCTC9	201	-----	-----	-----	250
BOVGSTA	201	cccccccccc	cccccccccc	cccccccccc	250
MUSGLYTN8	201	-----	CG	TCTTACGGAC	250
PCTC9	251	-----	-----	-----	300
BOVGSTA	251	AAACCCACGTG	TCTCTAGT	CCACGCCACG	300
MUSGLYTN8	251	CTTCTTCTTA	CTGGGGTGAC	ACCTTCTCTT	300
Exon 1 ↓ Exon 2					
PCTC9	301	-----	-----	-----	350
BOVGSTA	301	CTGGCATTTC	CTGGGAAACA	CCAGACACTT	350
MUSGLYTN8	301	CACTTACCA	TTCCTCTAA	GAATTCGGC	350
PCTC9	351	-----	-----	AGC	400
BOVGSTA	351	AAAGCTTCAAC	CTTCGGCTTC	CTCC-----AGC	400
MUSGLYTN8	351	ACCCCTTAC	CTTCTTTC	CTCTCTCT	400
PCTC9	401	ACACCTCACT	ACAACTT-GT	TTC-----GGC	450
BOVGSTA	401	GGAGCTCACT	ACAACTT-GG	TACTTTGGC	450
MUSGLYTN8	401	ACACCTCAAC	ACAACTTGG	TCTCTTCT	450
Exon 2 ↓ Exon 3					
PCTC9	451	ACGAGAGGAT	GAG-----	-----	500
BOVGSTA	451	ACGAGAGGAT	GAG-----	-----	500
MUSGLYTN8	451	ACCTGAGGAT	ACGCTCACT	CACTCTGCT	500
PCTC9	501	-----	-----	-----	550
BOVGSTA	501	-----	-----	-----	550
MUSGLYTN8	501	CTCTGGATT	AAACCCCTGT	ACCTACCTTC	550
PCTC9	551	-----	-----	-----	600
BOVGSTA	551	-----	-----	-----	600
MUSGLYTN8	551	ATCACTATGC	TTCAAGATCT	CCAGCTGAC	600

Fig 4 (cont) 4-2

PCTCD BOVGSTA MUSGLYTNs	601	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	Exon 3 ↓ Exon 4
	501	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	650
	601	CAAGTCACAA	ACAGACTCTTC	CTTCCTCAAC	ATCTCCATCA	CAACACAA	AA	AA	AA	AA	AA	AA	650
PCTCD BOVGSTA MUSGLYTNs	651	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	700
	651	TAATGATCT	CAACACAA	CTTCCTCTCT	CAATCTCTCT	CTCTCTCACT	CT	CT	CT	CT	CT	CT	700
	651	TAATGATCT	CAACACAA	CTTCCTCTCT	CAATCTCTCT	CTCTCTCACT	CT	CT	CT	CT	CT	CT	700
PCTCD BOVGSTA MUSGLYTNs	651	TAATGATCT	CAACACAA	CTTCCTCTCT	CAATCTCTCT	CTCTCTCACT	CT	CT	CT	CT	CT	CT	700
PCTCD BOVGSTA MUSGLYTNs	701	CTAAATGCTT	TCTTTTCCCA	ATACATCAAC	ACCCACAAAC	CTTCCTTCTT	CT	CT	CT	CT	CT	CT	750
	701	CTCATTGTTG	TCTTTTCCCA	ATATATCCAC	ACCCACAAAC	CTTCCTTCTT	CT	CT	CT	CT	CT	CT	750
	701	GTGTTGTCG	TCTTTTCCCA	ATATATCAAC	ACCCACAAAC	CTTCCTTCTT	CT	CT	CT	CT	CT	CT	750
PCTCD BOVGSTA MUSGLYTNs	751	CTGGATATAAC	CACTCAAA	ACCCACAACT	CTTCACACCC	CTTCACACCC	CT	CT	CT	CT	CT	CT	800
	751	CTGGATAAAC	CCATCAAA	ACCCACAACT	CTTCACACCC	ACCTTCACA	CT	CT	CT	CT	CT	CT	800
	751	CTGGATATAT	CACACAA	TTCCACAGCT	CTTCACACAA	AGATGGACAA	CT	CT	CT	CT	CT	CT	800
PCTCD BOVGSTA MUSGLYTNs	801	CTTCCTGCG	TTTCCTGACC	TCCTTTTAACT	ATCCACACTCA	CACTTACAC	CT	CT	CT	CT	CT	CT	850
	801	ACCCCTGCTG	CTTCCTGACA	TCCTTTTAACT	ATG-----	ATG-----	CT	CT	CT	CT	CT	CT	850
	801	ACGACTGCTG	CTTCCTGACC	TCCTTTTAACT	ATG-----	ATG-----	CT	CT	CT	CT	CT	CT	850
PCTCD BOVGSTA MUSGLYTNs	851	CAACACACAC	ACCTTATACG	CTACCAAAAG	CAACACAA	AAACACACAA	CT	CT	CT	CT	CT	CT	900
	851	CAACACACATC	CAACATAA	CTAACAAAG	CAACACAA	ACCAACACCA	CT	CT	CT	CT	CT	CT	900
	851	CAACACACAC	TAACACACCG	CTACCAAAAG	CTACACAA	CTACACACAT	CT	CT	CT	CT	CT	CT	900
PCTCD BOVGSTA MUSGLYTNs	901	CAACACACAC	CTTCGGCTAC	TCGACTGCTT	TAATCTGCTG	AAACCCCCAC	CT	CT	CT	CT	CT	CT	950
	901	---	ACCTTGTGAC	CTTAACCTAT	CGGACTGCTT	CAACCCATTT	AAACCCCCAC	CT	CT	CT	CT	CT	950
	901	---	TGAAACAC	CTTCACCTAT	CGGACTGCTT	CAATCCAAAC	AAACCCCCAC	CT	CT	CT	CT	CT	950
PCTCD BOVGSTA MUSGLYTNs	951	ACGCTGTGAC	CATAACCAAC	TCGAGGCTC	CACTGCTATG	GGAAAGGACT	CT	CT	CT	CT	CT	CT	1000
	951	ACGTTGTGAC	CATGACCAAC	TCGAGGCTC	CACTGCTATG	GGAAAGGACT	CT	CT	CT	CT	CT	CT	1000
	951	ATGTTTCAAC	ACTGACCCCC	TCGAGGCTC	CACTGCTATG	GGAAAGGACT	CT	CT	CT	CT	CT	CT	1000
PCTCD BOVGSTA MUSGLYTNs	1001	TACACACAG	CCCTCTTACA	TAATTTAAAT	CCACACACAA	AAATTAACCT	CT	CT	CT	CT	CT	CT	1050
	1001	TACACACAG	CCCTCTTACA	TAATTTAAAT	CCACACACAA	AAATTAACCT	CT	CT	CT	CT	CT	CT	1050
	1001	TATCACACAC	CTCTGCTGCA	AACTACTAC	CCACACACAA	AACTACTCT	CT	CT	CT	CT	CT	CT	1050
PCTCD BOVGSTA MUSGLYTNs	1051	CCCGCTGACC	CTTTTTCTCA	TCGCAACATA	CATTGACCAT	TACTTCAGG	CT	CT	CT	CT	CT	CT	1100
	1051	CCCGCTGACC	CTTTTCACCG	TCGCAACATA	CATTGACCAT	TACTTCAGG	CT	CT	CT	CT	CT	CT	1100
	1051	CCCGCTGACC	CTTTTTCTCA	TCGCAACATA	CATTGACCAT	TACTTCAGG	CT	CT	CT	CT	CT	CT	1100
PCTCD BOVGSTA MUSGLYTNs	1101	AGTTCTTAAAT	ATCTCCAAAT	ACATACCTCA	TCCTTGCCCA	CAACACATC	CT	CT	CT	CT	CT	CT	1150
	1101	AGTTCTTAAAC	CTCTGCTTAA	AAGCACTTCA	TCCTTGCCCA	CCCACTCATC	CT	CT	CT	CT	CT	CT	1150
	1101	AGTTCTTCAAC	CTCTGCTTCA	ATCTACCTCA	TCCTTGCCCA	TCCTTGCCCA	CT	CT	CT	CT	CT	CT	1150
PCTCD BOVGSTA MUSGLYTNs	1151	TTTTACATCA	TCCTGCTAC	TAATCTCAAC	ATCCCTTTCA	TAACGCTCCC	CT	CT	CT	CT	CT	CT	1200
	1151	TTTTATATCA	TCCTACATCA	TCCTGCTAC	ATCCCTTTCA	TAACGCTCCC	CT	CT	CT	CT	CT	CT	1200
	1151	TTTTACCTCA	TCATACATCA	CACTCCCGG	ATCCCTGCTC	TCCTACCTCA	CT	CT	CT	CT	CT	CT	1200
PCTCD BOVGSTA MUSGLYTNs	1201	TCCTCTCCCC	TCCTTTAAAC	TCTTTCACAT	CAACACACAC	AAACGCTCCC	CT	CT	CT	CT	CT	CT	1250
	1201	TCCTCTCCCC	TCCTTCACAG	TCTTTCACAT	CAACACACAC	AAACGCTCCC	CT	CT	CT	CT	CT	CT	1250
	1201	CCCTCTACAT	TCCTTCACAG	TCTTTCACAT	CAACACACAC	AAACGCTCCC	CT	CT	CT	CT	CT	CT	1250

Fig 4 (cont) 4-3

PCTCD	1251	ACACATCAAG CATGATGCCG ATGAAACCCA TCCGCGACCA CATTCTGCC	1300
BOVGSTA	1251	ACGACATCAAG CATGATGCCG ATGAAACCCA TCCGCGACCA CATTCTGCC	1300
MUSGLYTN5	1251	ACGATATCAAG CATGATGCCG ATGAAACCCA TTGGGACCA CATTCTGCC	1300
PCTCD	1301	CACATCCAGC ACCAGCTGGA CTTCCCTTC TCCATCCACG TCCATCAAGT	1350
BOVGSTA	1301	CACATCCAGC ATGACCTGA CTTCCCTTC TCCATCCACG TCCACCAAGT	1350
MUSGLYTN5	1301	CACATCCAGC ACCAGCTGGA CTTCCCTTC TCCATCCACG TCCATCAAGT	1350
PCTCD	1351	CTTCCAAAC AACCTTCCCG TCCAGACCTT CGCCAGCTCG CTCCCTCACCG	1400
BOVGSTA	1351	CTTCCAAACG AACCTTCCCG TCCAGACCTT CGCCAGCTCG CTCCCTCACCG	1400
MUSGLYTN5	1351	CTTCCAAAC AACCTTCCCG TCCAGACCTT CGCCAGCTCG CTCCCTCACCG	1400
PCTCD	1401	TACAGGGCTG CTGCTACAGG CCAGATCTCA ACAGATTCAC CTACGAGCC	1450
BOVGSTA	1401	TACAGGGCTG CTGCTACAGG CCAGATCCCA ATGACATTCAC CTACGAGCC	1450
MUSGLYTN5	1401	TCCAGGGCTG CTGCTACAGG CGCAGCTCCG ACAGATTCAC CTACGAGGG	1450
PCTCD	1451	CCCAGCCAGT CGCCAGCTTA CATTCGGTTT CGCCAGGGCG ATTTTTTATTA	1500
BOVGSTA	1451	CCCAGCCAGT CTCCAGCTTA CATTCGGTTT CGCCAGGGCG ATTTTTTATTA	1500
MUSGLYTN5	1451	CCCAGCCAGT CGCCAGCTTA CATTCGGTTT CGCCAGGGCG ATTTTTTATTA	1500
PCTCD	1501	CCACCCACCC ATTTTTGGG GAAACCCAC TCAACCTTCA AACATCACTC	1550
BOVGSTA	1501	CCATGCAGCC ATTTTTGGG GAAACCCAC TCAAGGCTTT AACATCACCC	1550
MUSGLYTN5	1501	CCACGGGGCC ATTTTTGGG GAAACCCCTAC TCAACATTCTC AACCTCACCA	1550
PCTCD	1551	AGGAGTCTTT CAAAGGAATC CTCCAGGACA AGAAAGATCA CATAAGAAGC	1600
BOVGSTA	1551	ACCAATGCTT CAAAGGAATC CTCAACGACA AGAAAGATCA CATAAGAAGC	1600
MUSGLYTN5	1551	GGGAGTCTTT TAAAGGGATC CTCCACCCACA AGAAAGATCA CATAAGAAGC	1600
PCTCD	1601	CACTCCATC ATGAAAGCC TCTAAACAG TATTTTCTTC TCAACAAACC	1650
BOVGSTA	1601	CAATCCATC ATGAAACCCCA TCTAAACAG TATTTTCTTC TCAACAAACC	1650
MUSGLYTN5	1601	CACTCCATC ATGAAACCCCA CCTCAACAAA TATTTCTTT TCAACAAACC	1650
PCTCD	1651	CACTAAATC TTATCCCCAG AATACCTG CGATTATCAT ATAGCCATCT	1700
BOVGSTA	1651	TACTAAATC TTATCCCCGG AATACCTG CGATTATCAC ATAGCCCTAC	1700
MUSGLYTN5	1651	CACTAAATC CTATCTCCAG AGTATCTG CGACTATCAC ATAGCCCTCC	1700
PCTCD	1701	CTCTCCATAT TACCATGTC AACATACCTT CGCAGAAAAA AGACTATATA	1750
BOVGSTA	1701	CTCCGGATAT TAACTGTC AACATGTCCTT CGCAGACAAA AGACTATATA	1750
MUSGLYTN5	1701	CTTCACATAT TAAAGCTGTC AACGCTACCTT CGCAGACAAA AGACTATATA	1750
STOP			
PCTCD	1751	TTGGTTACAA ATAACTCTG ACTTAAATT CTGCCACCAAT TTTTCTGAAAT	1800
BOVGSTA	1751	CTGGTTACAA ATAACTCTG ACTT-----T CTGCCACCAAT TTTTCTGAAAT	1800
MUSGLYTN5	1751	TTGGTTACAA ATAACTCTG ACTTCACAAATT GTG----- --ATGGAAAC	1800
PCTCD	1801	TTGAAACAGT ATTAACCTGG CTACTTCTTC AGACAACTAC ---CACTAA	1850
BOVGSTA	1801	TTGACAGACT ATTAATCTGG CTACTTCTTC AGAAACATCA ---CACTAA	1850
MUSGLYTN5	1801	TTGACAC--- ATTAACCTGG CTACTTCTTC AGACAACTAC GAAACATCA	1850

Fig. 4 (cont) 4 - 4

PCTC	1851	TTTTAATTTT TAAAGGATAA CTAACTAA- ---TACCA CACACTAA-G	1900
BOVGSTA	1851	TTTTAATTTA AAAAAATAA CTAACTAA- ---TACCA CACACTAA-A	1900
MUSGLYTNs	1851	TTTCAGCTTT TAAAGAA-A CTAACTAAAC CAAACCCAC TACCATGCCA	1900
PCTC	1901	TACATATTTAT TCTCTCTTC AGCTTCTGAC CTTCGCAAT CCGCAATCA	1950
BOVGSTA	1901	TACATATTTAT TCTCTCTTC AGCTTCTGAC CTTCGCAATAC CCGCAATCA	1950
MUSGLYTNs	1901	AAACACATGAT TCTCTCT-CA CACCTCTGAC CT-CTATATAT CTCACGAA	1950
PCTC	1951	CTCTATGCCA ---TAACTCA TCTAAATTC CACTCATTTC .....	2000
BOVGSTA	1951	ACCTCTGG ---TAACTCA TCTAAATTC CACTCATTTC TAACTATTC	2000
MUSGLYTNs	1951	CTCTATGCCA AGTAATCAGG TATAAATTC CAAATTTTC TAACTATTC	2000
PCTC	2001	.....	2050
BOVGSTA	2001	TTCTCTTCG CCGGGGGGAA TCCATACAC ATCTGTTAA CC.....	2050
MUSGLYTNs	2001	TCCTCTTCG AAGCTTCA TCTACAAAT CAAATTTAA TTGACAAAGC	2050
PCTC	2101	.....	2100
BOVGSTA	2101	.....	2100
MUSGLYTNs	2101	AAACACACAT GCGGAAATCT TCTTCCAGT CTCTATACA ATTCACCACT	2100
PCTC	2151	.....	2150
BOVGSTA	2151	.....	2150
MUSGLYTNs	2151	TCGACCGCTC CATCCCTTC CCTTCATAT CTCTCTTC AGTGGACATT	2150
PCTC	2201	.....	2200
BOVGSTA	2201	.....	2200
MUSGLYTNs	2201	TAAAGGAAAC CAGACACCTT TTGACCCAG AGACCTTAA TAAAGGATCC	2200
PCTC	2251	.....	2250
BOVGSTA	2251	.....	2250
MUSGLYTNs	2251	AACTCTACCA TCACTCTTA AAACCTGATG CCTCCACCGA CGCTCCACT	2250
PCTC	2301	.....	2350
BOVGSTA	2301	.....	2350
MUSGLYTNs	2301	CCAGGGCCCA CTACGCTATT CTTCCTCTCC TCCCTATAA CGACGCAAC	2350
PCTC	2351	.....	2400
BOVGSTA	2351	.....	2400
MUSGLYTNs	2351	ACTCCCAATA CCTACTTTTCG TCCACATGT TCACTCTCA CGAAATCA	2400
PCTC	2401	.....	2450
BOVGSTA	2401	.....	2450
MUSGLYTNs	2401	ACGCTCAAA CTTACACGGA CATAACACTT CGGTTGCTA ATTCACCA	2450
PCTC	2451	.....	2500
BOVGSTA	2451	.....	2500
MUSGLYTNs	2451	CTTACAAACA CACACACCTT TCTTCACGAT GACTAACACC AGCAATTGA	2500

Fig. 4 (cont.) 4 - 5

PCTCD	2501 .....	2550
BOVGSTA	2501 .....	2550
MUSGLYTN5	2501 TCCAACTGTG TTTCATTTTC TTTTCCCCAA ATTTGATTCGA TCTCTCTTACG	2550
PCTCD	2551 .....	2600
BOVGSTA	2551 .....	2600
MUSGLYTN5	2551 TTTCGTGTTT CACCCCTGTC CACACCTCTT CACTGATCA CGGAACTACA	2600
PCTCD	2601 .....	2650
BOVGSTA	2601 .....	2650
MUSGLYTN5	2601 CTACCTCAAC CGACTCAACG CGACACCTT ATTTATATACG AACACATCT	2650
PCTCD	2651 .....	2700
BOVGSTA	2651 .....	2700
MUSGLYTN5	2651 CTCACTCTCA CCTCTTACCT ACACCTCTT CTGAACTTCC CAGTTCTCA	2700
PCTCD	2701 .....	2750
BOVGSTA	2701 .....	2750
MUSGLYTN5	2701 ACCCTATGTC TTCCACCTCTA CGCCCTCTCA TCCACCCCTT CACTCAACAC	2750
PCTCD	2751 .....	2800
BOVGSTA	2751 .....	2800
MUSGLYTN5	2751 AAAACCCCTT CTACATCAAC CTCATTTCCC CCTCTTACTT ACTTATACAA	2800
PCTCD	2801 .....	2850
BOVGSTA	2801 .....	2850
MUSGLYTN5	2801 TCTGACGGC AACCCGCGAC ATCTACCTGG CACCATACCA ACCGATTTA	2850
PCTCD	2851 .....	2900
BOVGSTA	2851 .....	2900
MUSGLYTN5	2851 TGGCAATGGG AACCCGAGTC ATCTACAAAGG ACCCTCTCA CCTCTCTTC	2900
PCTCD	2901 .....	2950
BOVGSTA	2901 .....	2950
MUSGLYTN5	2901 CGCCCTCTCA CGCTCTGGG CGACCCCTGT ATAGCTGCTT CTCAACCTAT	2950
PCTCD	2951 .....	3000
BOVGSTA	2951 .....	3000
MUSGLYTN5	2951 CGCTCCCGAC CCTTTGGCA ATCTTAAAT GACCTTTCG CACCTGCCC	3000
PCTCD	3001 .....	3050
BOVGSTA	3001 .....	3050
MUSGLYTN5	3001 CTAACACCCCT TAAACACAT ATCTTAAATC ACCTCTACTG CTAACAGTAA	3050
PCTCD	3051 .....	3100
BOVGSTA	3051 .....	3100
MUSGLYTN5	3051 CACAAATTACA CTTATCAAAT AACAAAGGAA ATAAATTCTCC CCTTCTCTC	3100

Fig 5

PSM Line-up (aa):

	Ex 4 ↓ Ex 5	Ex 5 ↓ Ex 6
PCT(Frame 1)	1 MNVKGRVVL SLLVSTVMVV PHEYINSPCG SLTHIYQSKN PEVCG-SGAQR	50
BCT(Frame 1)	1 MNVKCKVILS MLVYSTVIVV PHEYINSPCG SLTHINPSRN PEVCGSSIQK	50
MCT(Frame 1)	1 MNVKCKVILL MLIVSTVVVV PHEYVNSPDG SPLHIYHTK1 PEVGENRHQK	50
	Ex 6 ↓ Ex 7	Ex 7 ↓ Ex 8
PCT(Frame 1)	51 GWNFPFWFNN CTNSYNEEED AIGNEKZQRK EDNRCZLPLV DWFNPEKRP2 100	
BCT(Frame 1)	51 GWNLPFWFNN C---YKEEDG DINEEKEQRN ED-ESXLLKS DWFNPTKRP2 100	
MCT(Frame 1)	51 DWHFPFWFNN CTHGYQEDHV EGRRREK-CRN GDRIEEPQLW DWPNPKNRD2 100	
	Ex 8 ↓ Ex 9	
PCT(Frame 1)	101 AVTITRKAP VVHECTYNRA VLDDYYAKQK ITVGLTVFAV CRYIEHYLEZ 150	
BCT(Frame 1)	101 VVTHTKWKAP VVHECTYNRA VLDDYYAKQK ITVGLTVFAV CRYIEHYLEZ 150	
MCT(Frame 1)	101 VLTVTTPWKAP IVHECTYDTA LLEKYYATQK ITVGLTVFAV CRYIEHYLED 150	
PCT(Frame 1)	151 FLISANTYFH VCHXVIPYIH VCDISGRMPLI ELOPLASRPFV FRIKSEKRHQ 200	
BCT(Frame 1)	151 FLTSANKHFI VCHBVIPIYIH VCDVGRMPLI ELOPLASRPFV FRIKPEKRHQ 200	
MCT(Frame 1)	151 FLESADMYFH VCHRVIFYIH IDDTSGRMPPV KLNPLXSLQV FEIRSEKRHQ 200	
PCT(Frame 1)	201 DISMMRMIKTI GEHLNHIQH EVDLFLFCMDV DQVFQNNFGV ETLGQSVQL 250	
BCT(Frame 1)	201 DISMMRMIKTI GEHLVHIIQH EVDLFLFCMDV DQVFQDKFGV ETLGZSVQL 250	
MCT(Frame 1)	201 DISMMRMIKTI GEHLNHIQH EVDLFLFCMDV DQVFQDNFGV ETLGQLVQL 250	
PCT(Frame 1)	251 QAHWYKAHPD EFTYERRKES AAYIPFCQCD FYYHAAIFCG TPTQVLNITQ 300	
BCT(Frame 1)	251 QAHWYKAHPD EFTYERRKES AAYIPFCQCD FYYHAAIFCG TPTQVLNITQ 300	
MCT(Frame 1)	251 QAHWYKASPE KFTYERRELS AAYIPFCGCD FYYHAAIFCG TPTHILNITR 300	
PCT(Frame 1)	301 ECFKGILQOK ENDIEAEWHD ESHLNKYLIL NKPTKILSPE YCWDYHIGMS 350	
BCT(Frame 1)	301 ECFKGILQDK KNDIEAQHHD ESHLNKYFLL NKPTKILSPE YCWDYHIGLP 350	
MCT(Frame 1)	301 ECFKGILQDK KHDIEAQHID ESHLNKYFLP NKPTKILSPE YCWDYQIGLP 350	
PCT(Frame 1)	351 VDIRIVKIAN QKEYNLVRN NI*..... 400	
BCT(Frame 1)	351 ADIKLVIQMSH QKEYNLVRN NV*..... 400	
MCT(Frame 1)	351 SDIKSVKVAH QKEYNLVRN NV*..... 400	

Fig. 6.

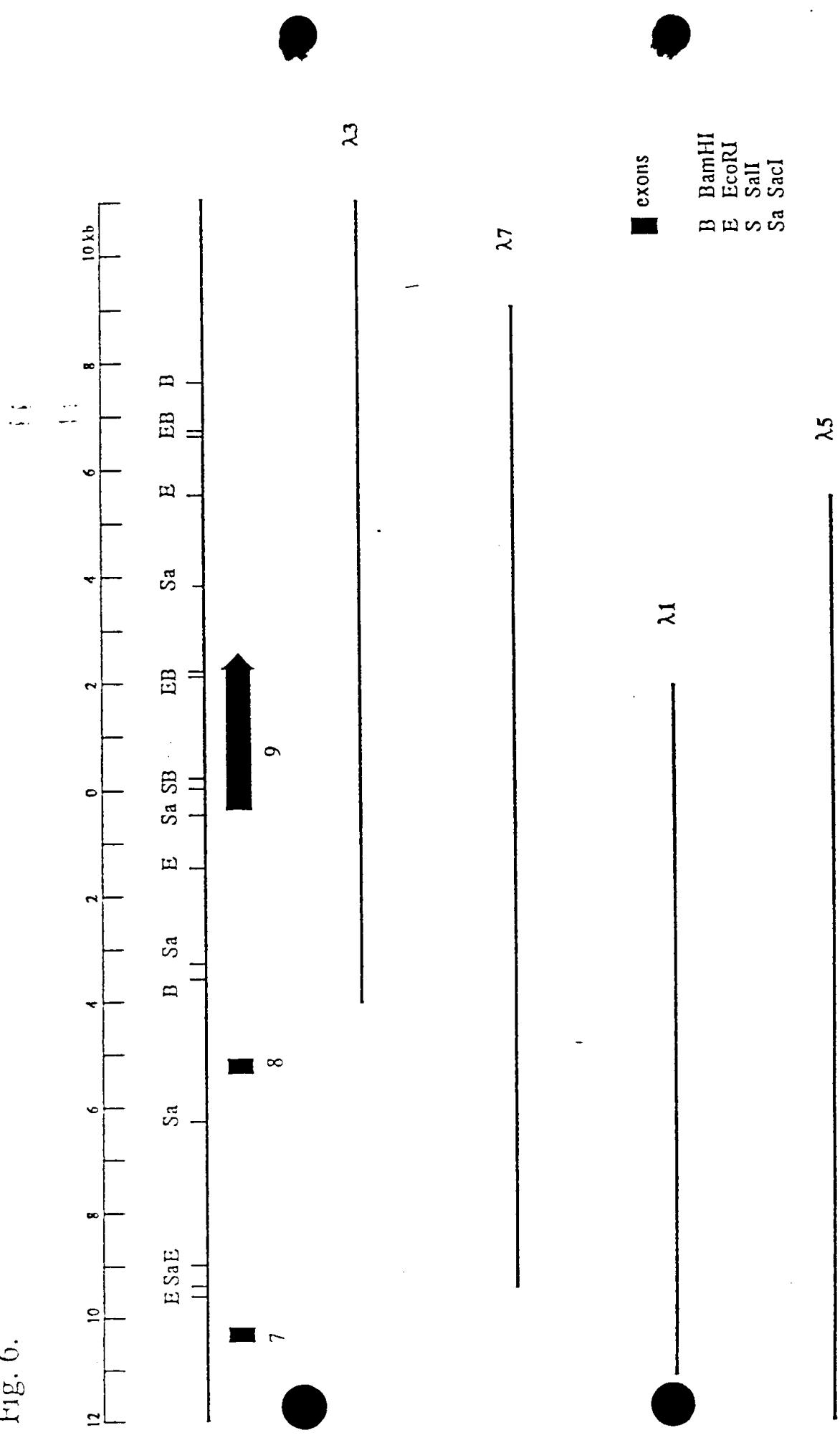
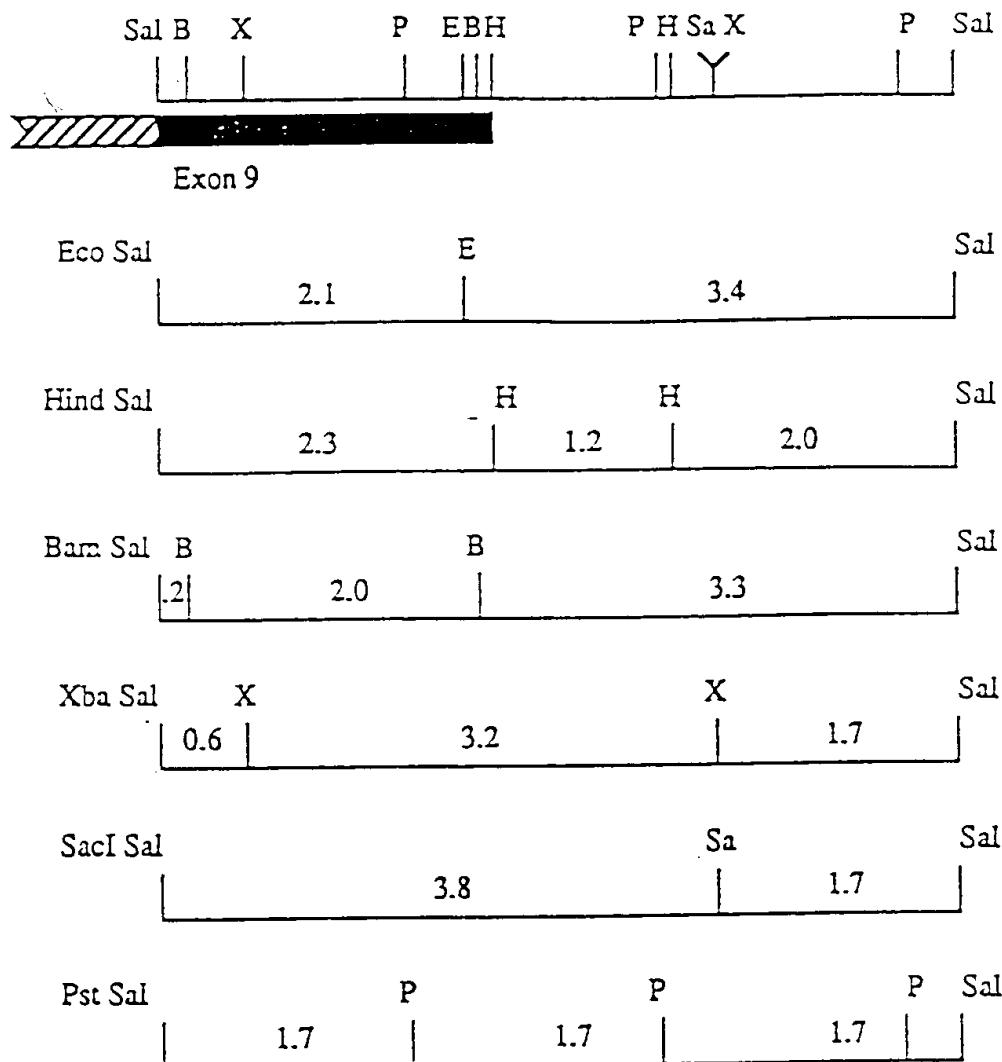


Fig. 7

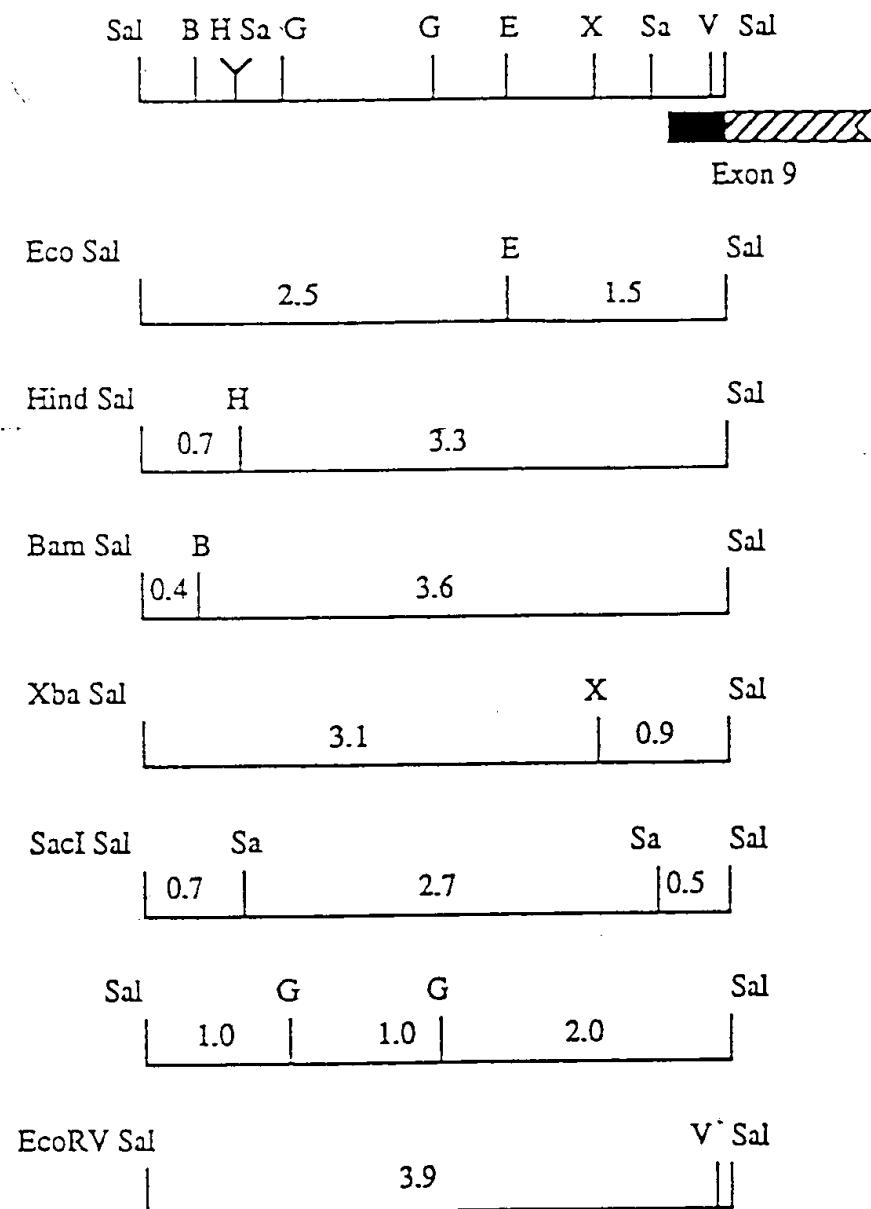


A	ApaI
B	BamHI
C	ClaI
E	EcoRI
G	BglII
H	HindIII
K	KpnI
N	NotI
P	PstI
S	SalI
Sa	SacI
V	EcoRV
X	XbaI
Xh	XbaI

No sites for: BglIII, Nde, PvuI, XbaI, Kpn, SacII, EcoRV, SmaI, ClaI, ApaI, Not

pBS+KS:

.... SacI SacII Not XbaI Spe Bam SmaI PstI EcoRV Hind ClaI SalI XbaI ApaI Kpn ....



A	ApaI
B	BamHI
C	ClaI
E	EcoRI
G	BglII
H	HindIII
K	KpnI
N	NotI
P	PstI
S	Sal
Sa	SacI
V	EcoRV
X	XbaI
Xh	XbaI

No sites for: Nde, PvuI, Xba, Kpn, SacII, Sma, Cla, Apa, Not

Unmapped sites for: Pst, PvuII

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xba Apa Kpn ...

Fig. 9

[ 1 kb ]

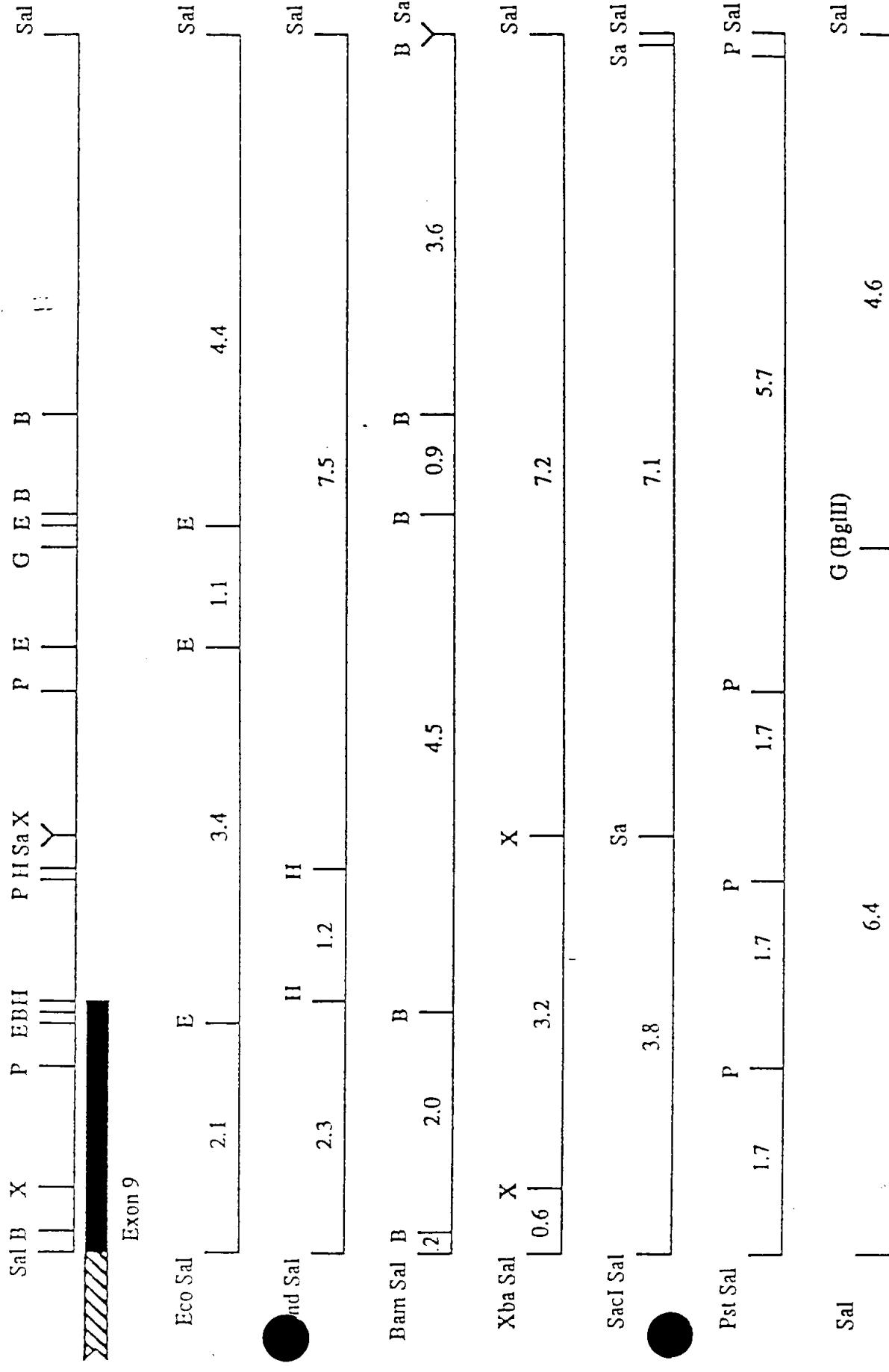


Fig. 9 (cont)

No sites for:  $Xho$ ,  $Kpn$ ,  $SacII$ ,  $Sma$ ,  $Cla$ ,  $EcoRV$ ,  $\lambda pa$ ,  $Not$ ,  $PvuI$ ,  $NdeI$   
pUBS:  
.....  $SacI$   $SacII$   $Not$   $XbaI$   $SpeI$   $Ban$   $Sma$   $PstI$   $EcoRV$   $Hind$   $Cla$   $Sal$   $XbaI$   $\lambda pa$   $Kpn$  ....

$\lambda$   $\lambda paI$   
B  $BamHI$   
C  $Clal$   
E  $EcoRI$   
G  $DgII$   
H  $HindII$   
K  $KpnI$   
N  $NolI$   
P  $PstI$   
S  $Sal$   
 $S^a$   $SacI$   
V  $EcoRV$   
X  $XbaI$   
 $X^h$   $XhoI$

Fig. 10

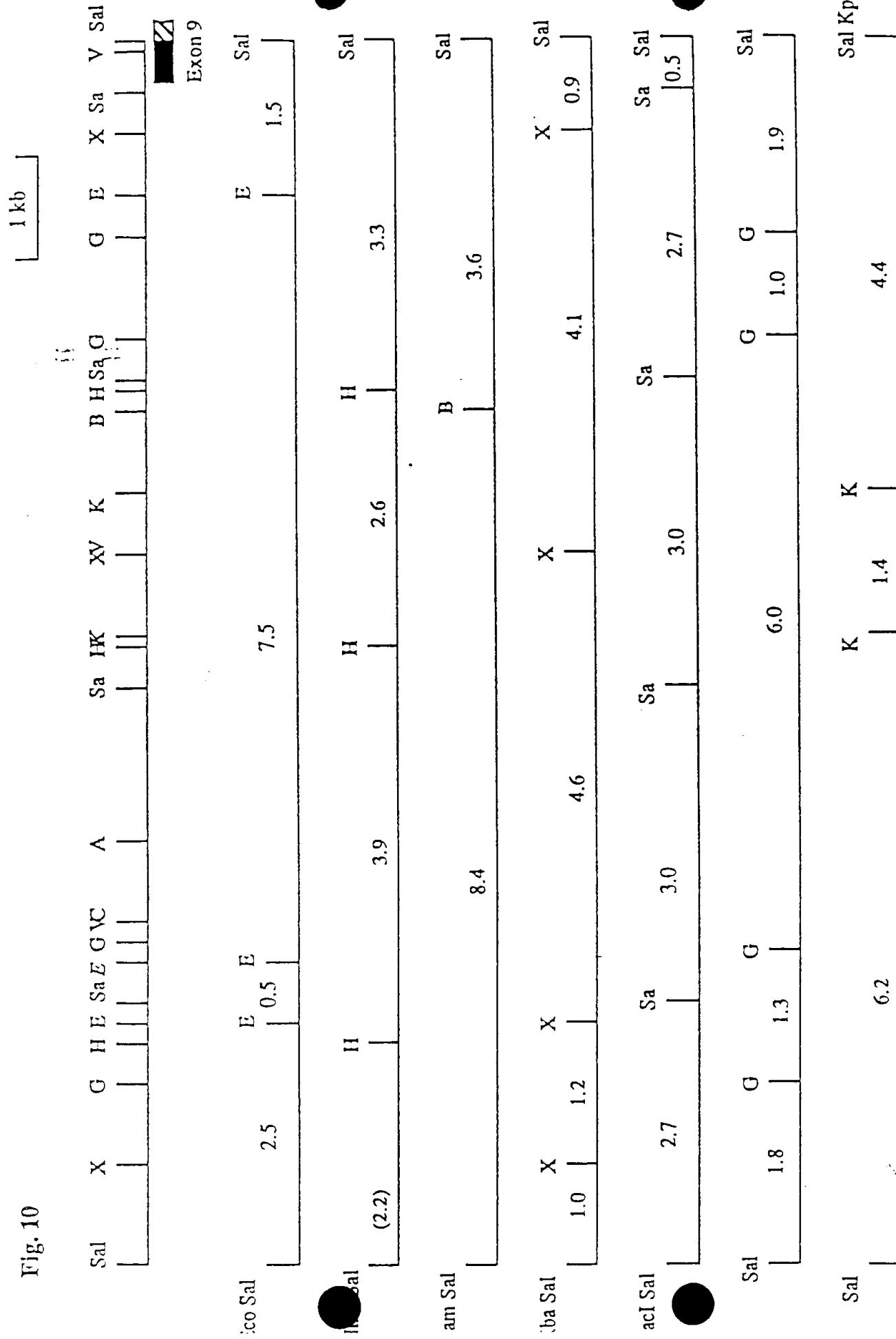
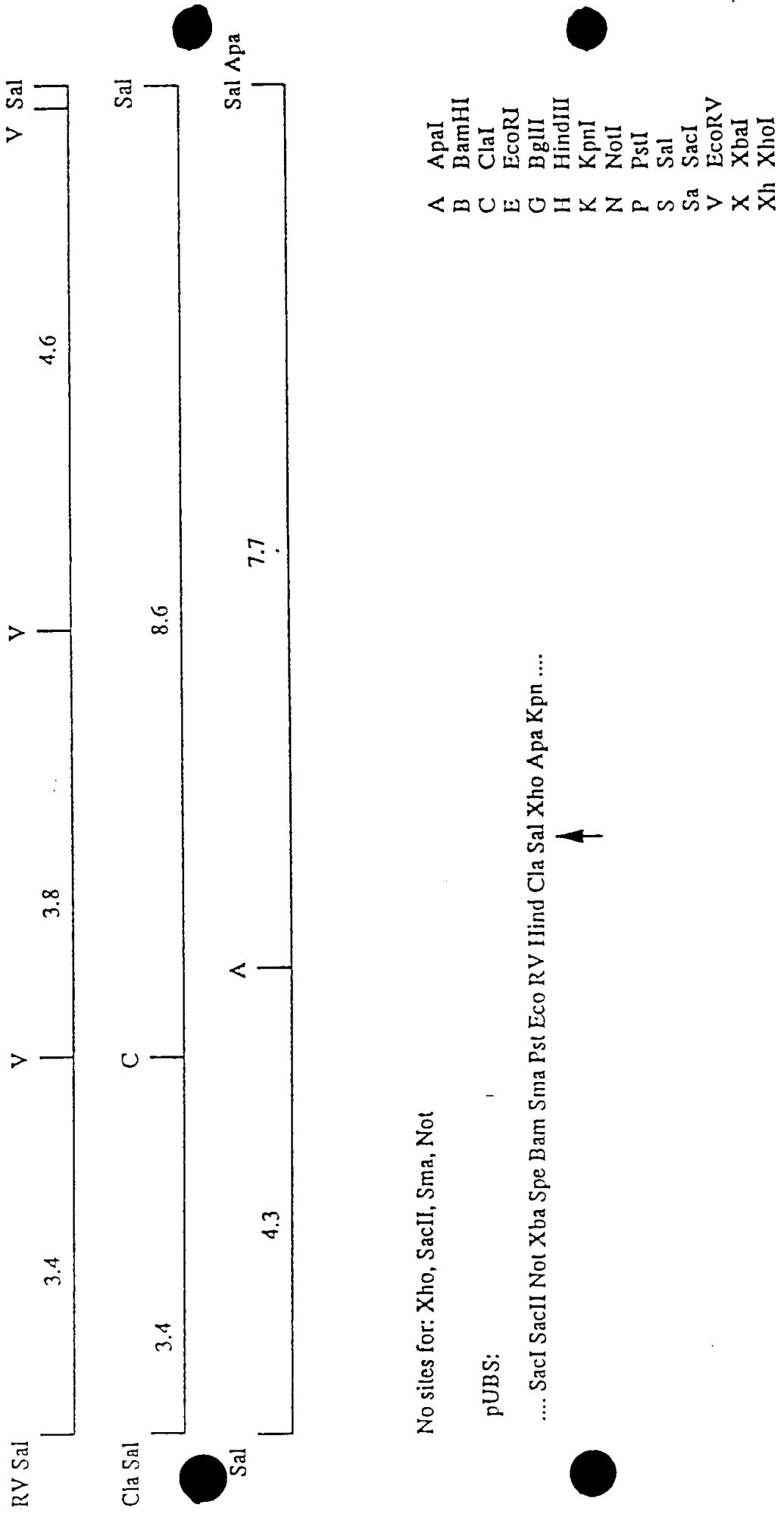
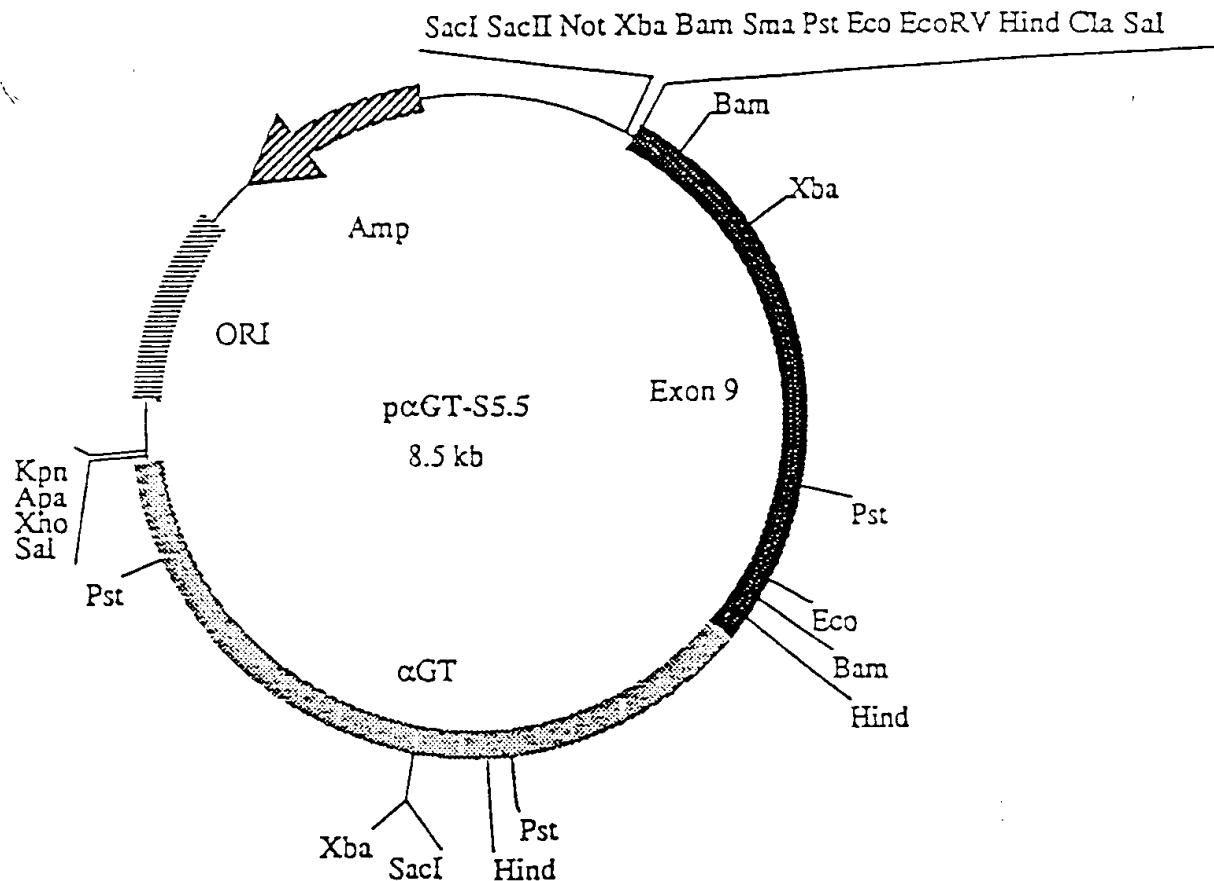
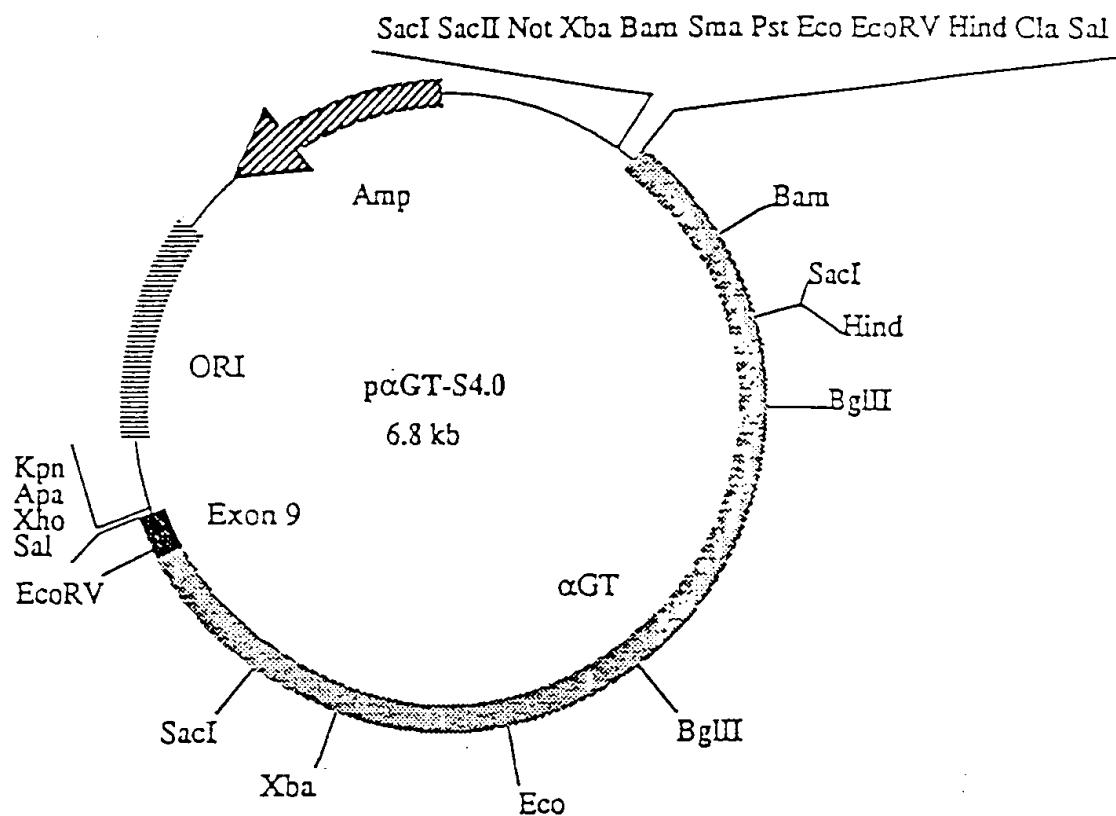


Fig. 10 (cont)





- $\alpha$ 1,3 galactotransferase ( $\alpha$ GT) non-coding DNA
- Exon 9 of  $\alpha$ GT
- Neo resistance gene
- Bacterial origin of replication
- Amp resistance gene



-   $\alpha$ 1,3 galactotransferase ( $\alpha$ GT)  
non-coding DNA
-  Exon 9 of  $\alpha$ GT
-  Neo resistance gene
-  Bacterial origin of replication
-  Amp resistance gene

Fig. 13

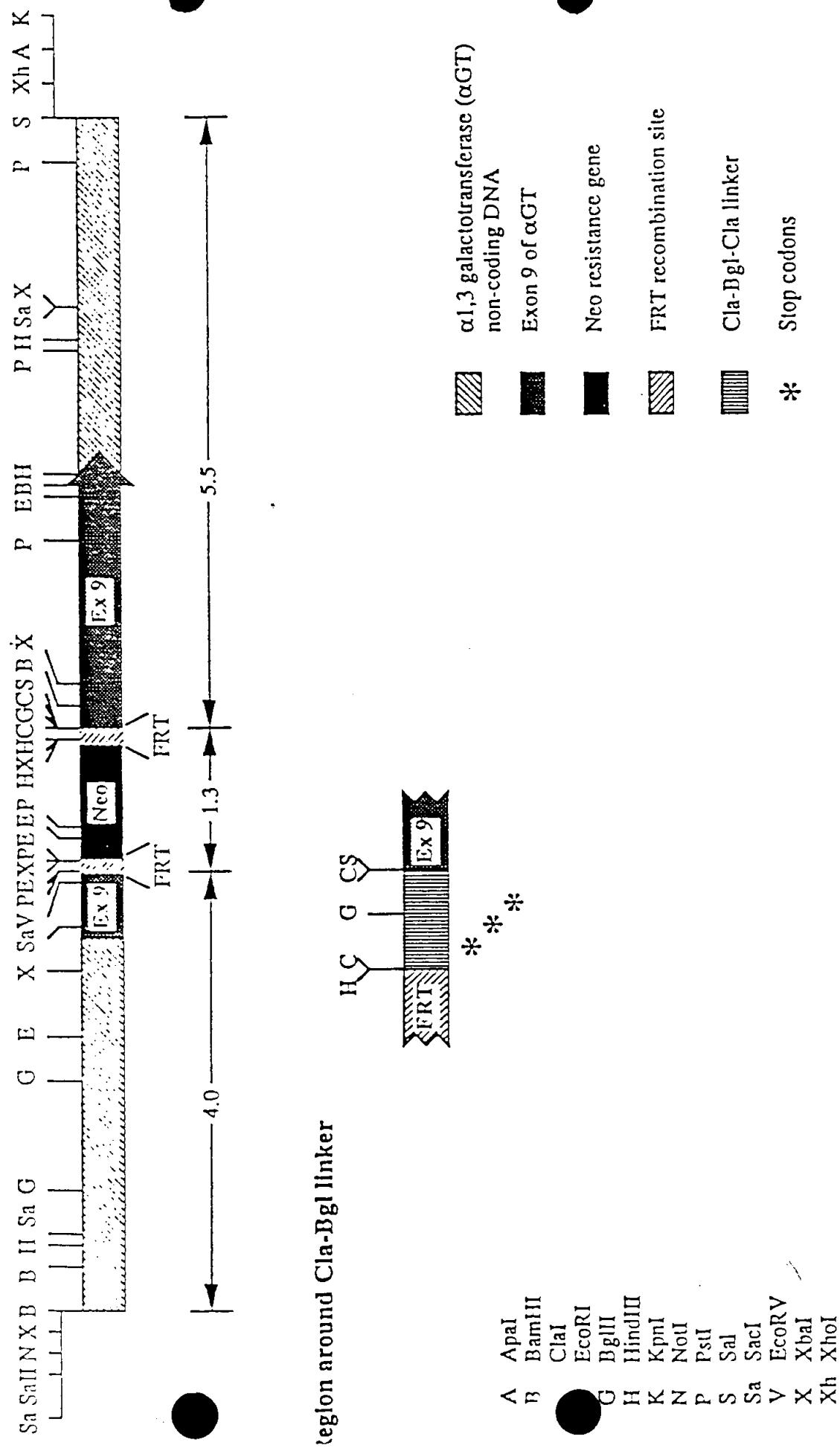


Fig. 14

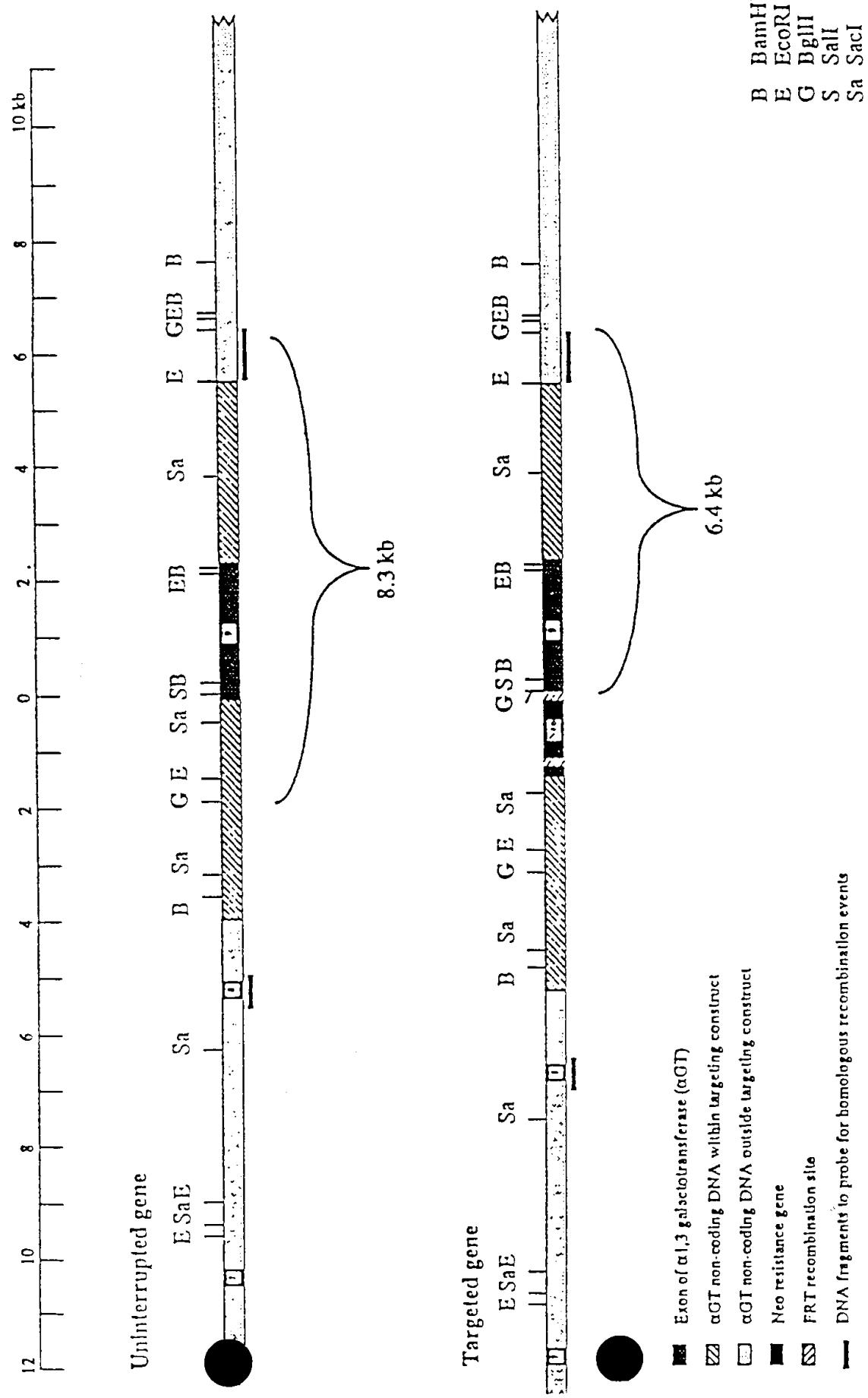
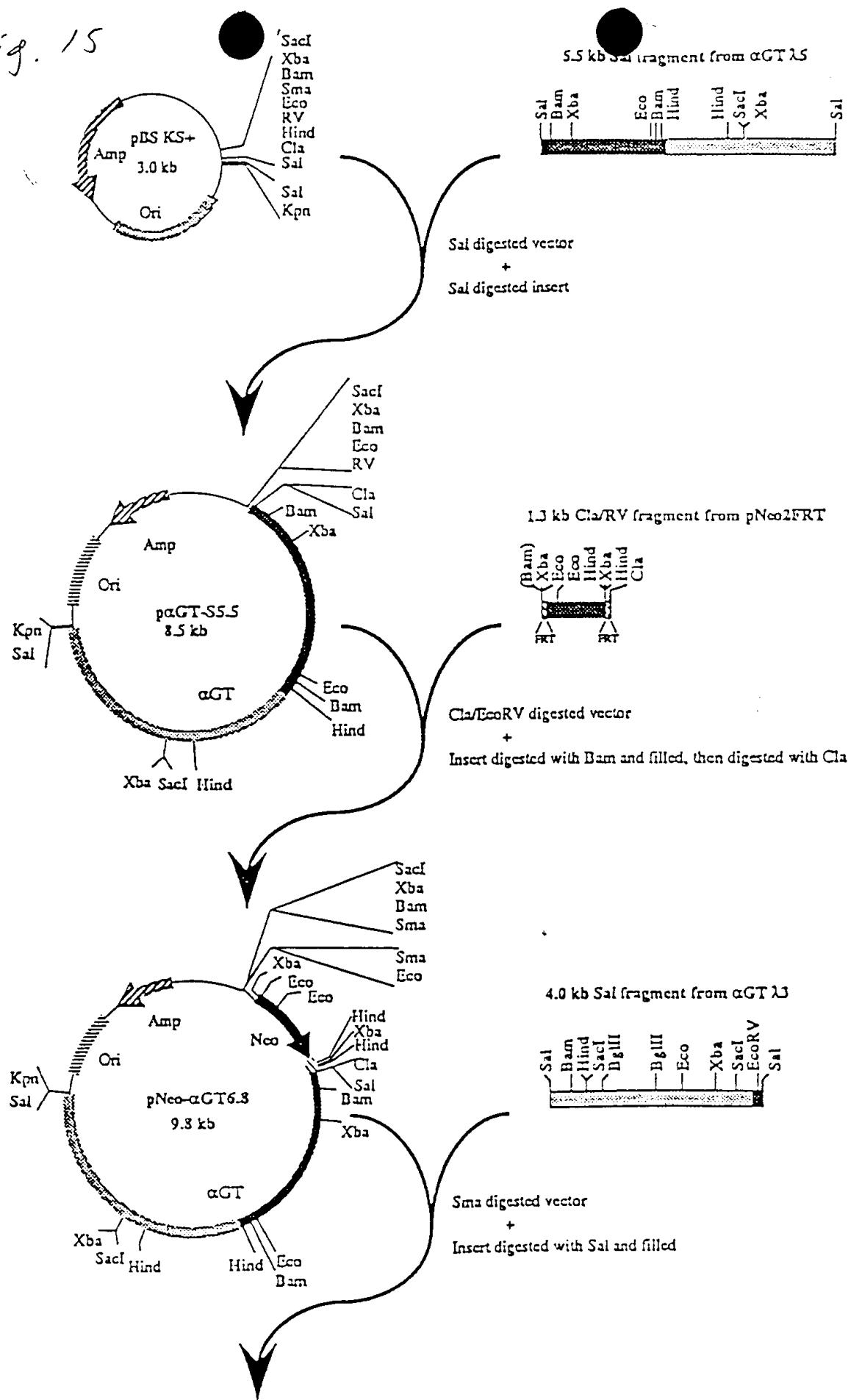
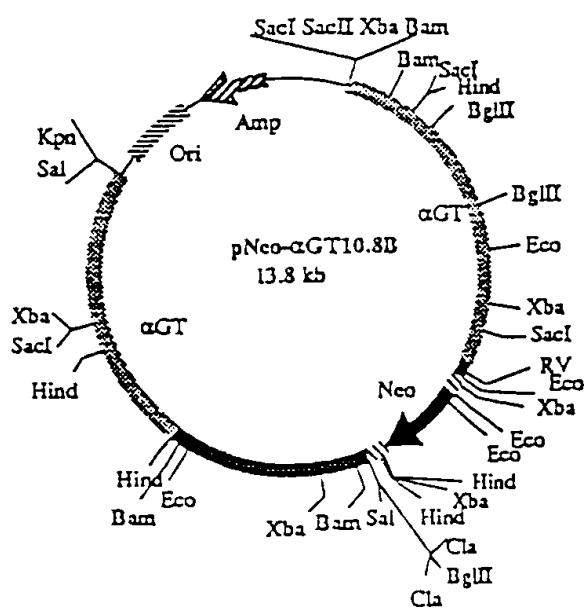
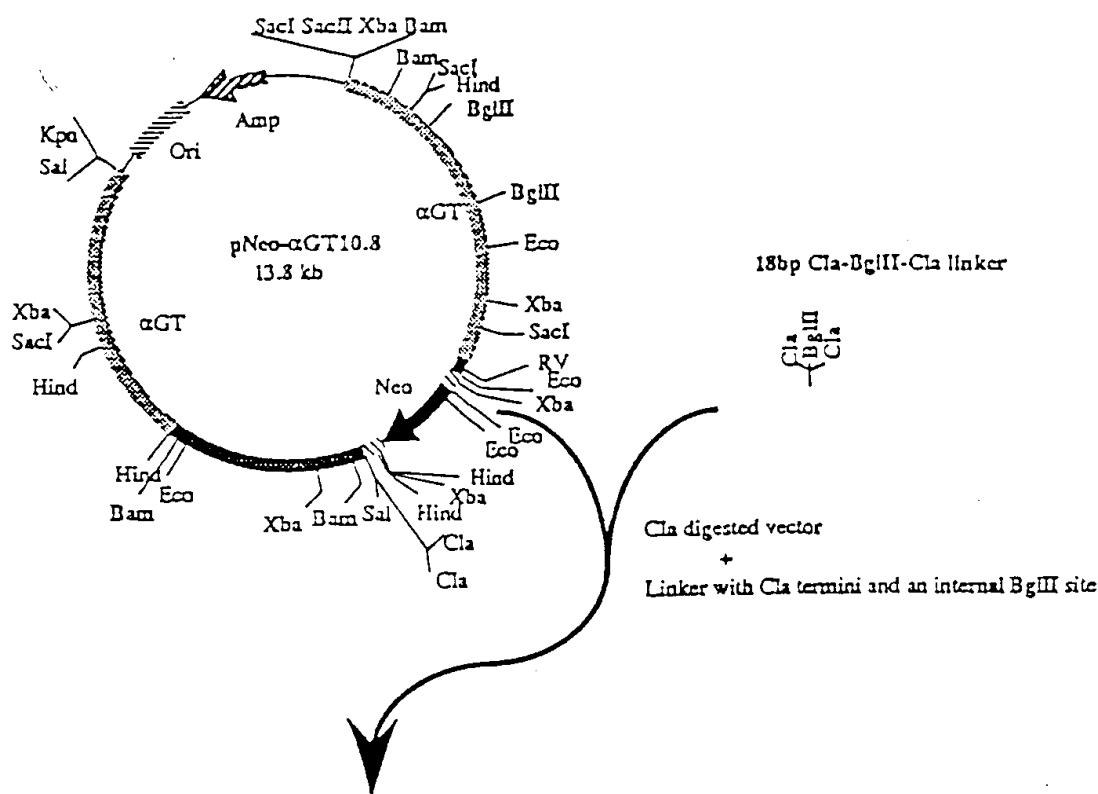


Fig. 15





- α1,3 galactosyltransferase (αGT) non-coding
- Exon 9 of αGT
- Neo resistance gene
- FRT recombination site
- Bacterial origin of replication
- Amp resistance gene

Fig. 16

10 20 30 40 50 60  
CAAGGGCTCCA CGAAATTCGAT GATCCCCCAG CTTGAAAGTTC CTATTCGGAA GTTCGTTTC  
70 80 90 100 110 120  
TCTAGAAAGT ATAGGAACCTT CAAGCTGGGC TGCAGGAATT CGATTCGAGC AGTGCTGGTTT  
130 140 150 160 170 180  
TCCAAAGAGGA ACCAAAAAAAGC CTCTCCACCC AGGCCTGGAA TGTTCACCCAG CAATGGCTAG  
190 200 210 220 230 240  
CACTGTGGTT TTGCAAGAGG AAGCAAAAAG CCTCTCCACCC CAGGCCTGGAA ATGTTTCAC  
250 260 270 280 290 300  
CCAAATGTCGA CGAAACCCCCG CCCAGGCTCT TGTCAATTGGC GAATTGAAAC ACCGAGAGCC  
310 320 330 340 350 360  
AGTCGGGGCG GCGCGGTCCC AGGTCCACTT GGCAATTTAA GGTGACGGGT GTGGCCCTGA  
370 380 390 400 410 420  
ACACCGAGCG ACCCTGCAGC CAATATGGGA TCGCCCATTG AACAAAGATGG ATTGGACCCA  
430 440 450 460 470 480  
GGTTCTCCCG CCCGTTGGGT GGAGAGGCTA TTCCGGCTATG ACTGGGCRCR ACAGACACCC  
490 500 510 520 530 540  
GGCTGCTCTG ATGCCCGCGT GTTCCGGCTG TCAGGGCAGG GCGGCCCCGT TCTTTTGTG  
550 560 570 580 590 600  
AACACCGACC TGTCCGGTGC CCTGAATGAA CTCCAAAGACG AGGCAGGGCG GCTATCGGG  
610 620 630 640 650 660  
CTGCCAACGA CGGGCGTTCC TTGGCCAGCT GTGCTCGACG TTGTCACTGA AGCGGGAAAG  
670 680 690 700 710 720  
GACTGGCTGC TATTGGCGGA AGTGGCCGGGG CAGGATCTCC TGTCACTGA CCTTGCTCTT  
730 740 750 760 770 780  
GCCGAGAAAG TATCCATCAT GGCTGATGCA ATGCGGGCGC TGCATAAGCT TGATCCCGCT  
790 800 810 820 830 840  
ACCTGCCCAT TCGACCACCA AGCGAAACAT CCCATCGAGC GAGCACGTCAC TCGGATGGAA  
850 860 870 880 890 900  
GCCGGCTTTC TCGATCAGGA TGATCTGGAC GAAGACCACG AGGGGCTTCC GCCAGCCGA  
910 920 930 940 950 960  
CTGTTGCCA GGCTCAGGGC GCGGATGCC GACGGCGAGG ATCTCGCTGT GACCCATGGC  
970 980 990 1000 1010 1020  
GATGCCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT TTTCTGGATT CATGGACTGT  
1030 1040 1050 1060 1070 1080  
GGCCCGCTGG GTGTGGCGGA CCCCTATCAG GACATAGCGT TGGCTACCCG TGATATGGCT  
1090 1100 1110 1120 1130 1140  
GAAGAGCTTG GCGGCGAATG GCCTGACCGC TTCTCTGGTC TTTACGGTAT CGCCGGCTCCC  
1150 1160 1170 1180 1190 1200  
GATTCGGAGC GCATCGCCCTT CTATCGCCCTT CTTGACGAGT TCTTCTGAGG GGATCGGGAA  
1210 1220 1230 1240 1250 1260  
TAAAAAGACA GAATTAAGCG CACGGGTGTT GGGCGTTGT TCCGATGATC AAGCTTGAG

Fig. 16 (cont'd)

1270 1280 1290 1300 1310 1320  
TTCCTTATTCC GAAGTTCTTA TTCTCTAGAA AGTATAGGAA CTTCAAGCTT ATCGATGAGT  
1330 1340 1350 1360 1370 1380  
AGATCTTGAT CGATACCGTC .....

Linker sequences : 0-28

FRT : 29-104

Polyoma virus enhancer repeats : 105-249

Herpes Simplex Virus Tyrosine Kinase promoter : 250-385

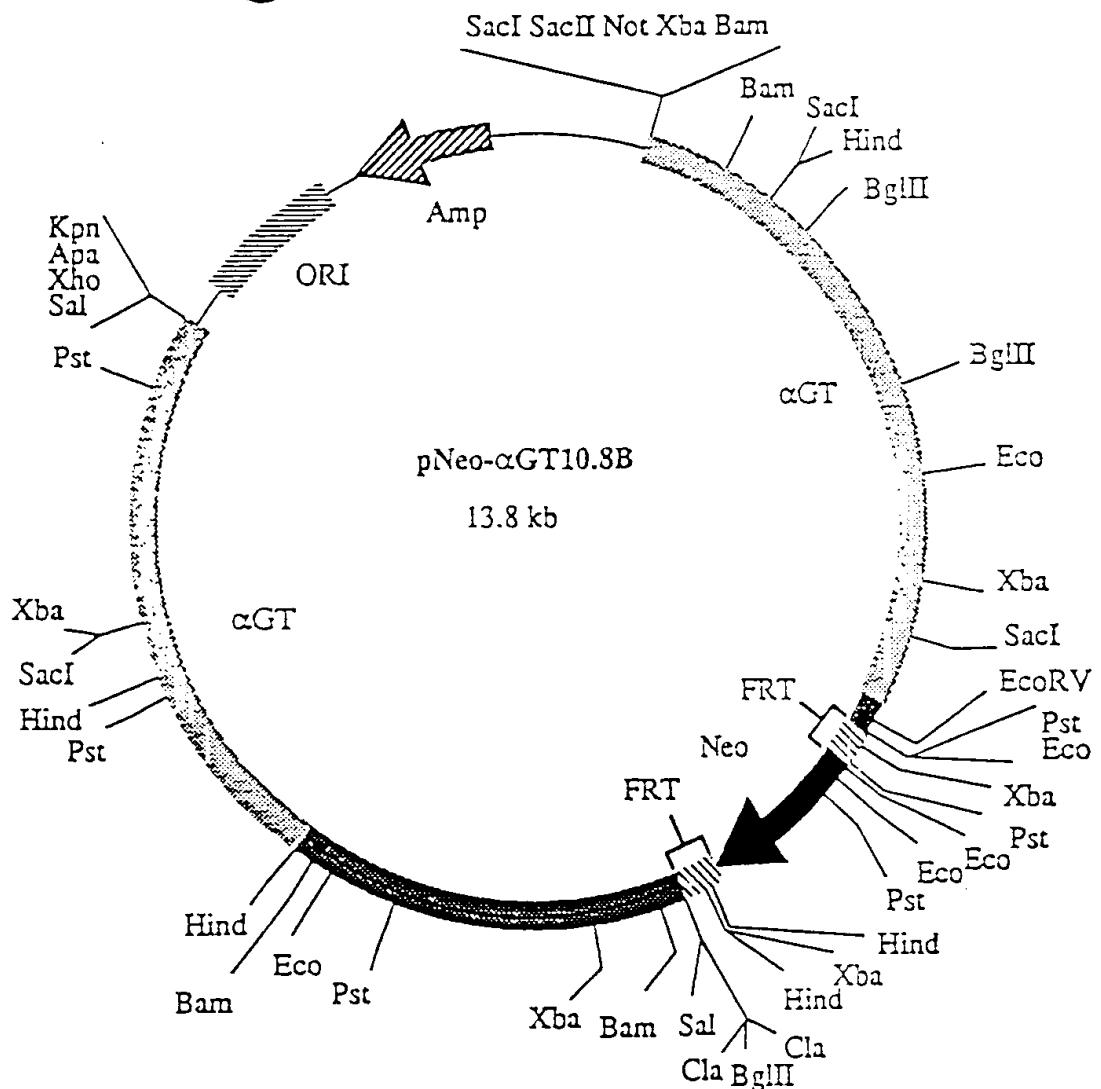
Neomycin phosphotransferase coding region : 385-1188

Herpes Simplex Virus Tyrosine Kinase PolyA signal : 1189-1249

FRT : 1250-1310

Linker sequences : 1311-1340

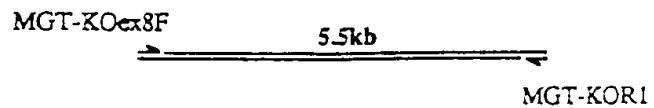
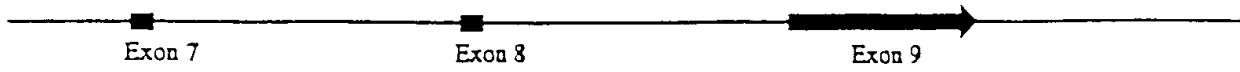
Fig. 17



- $\alpha$ 1,3 galactotransferase ( $\alpha$ GT) non-coding DNA
- Exon 9 of  $\alpha$ GT
- Neo resistance gene
- FRT recombination site
- Bacterial origin of replication
- Amp resistance gene

Fig. 17

Uninterrupted gene



Targeted gene

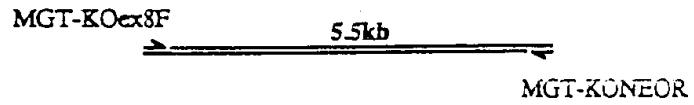
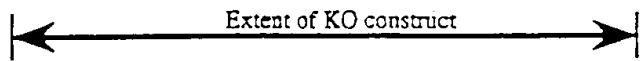


Fig. 18

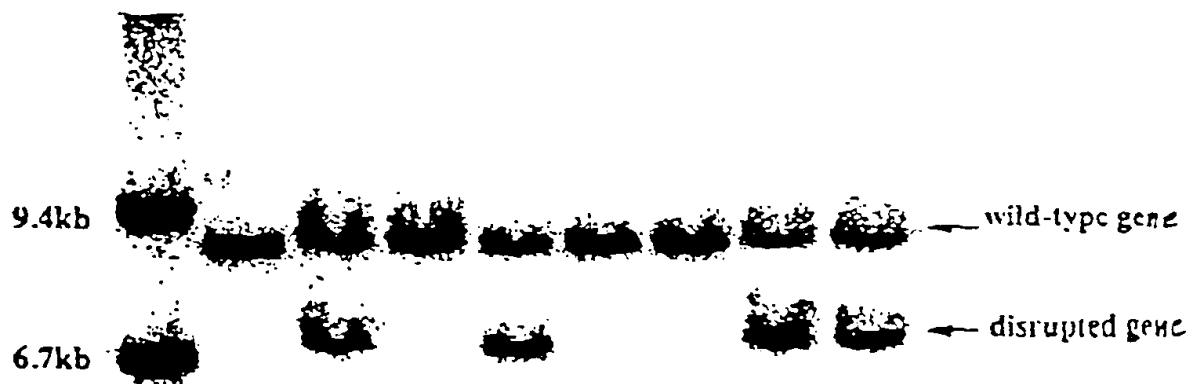
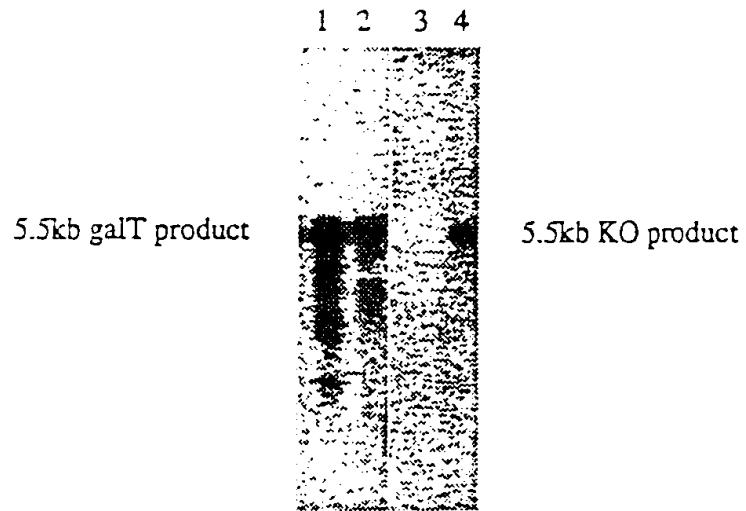


Fig.



1. CBAC template; wild type primers
2. 7C2 template; wild type primers
3. CBAC template; KO primers
4. 7C2 template; KO primers

Fig. 2 /

Uninterrupted gene



Targeted gene

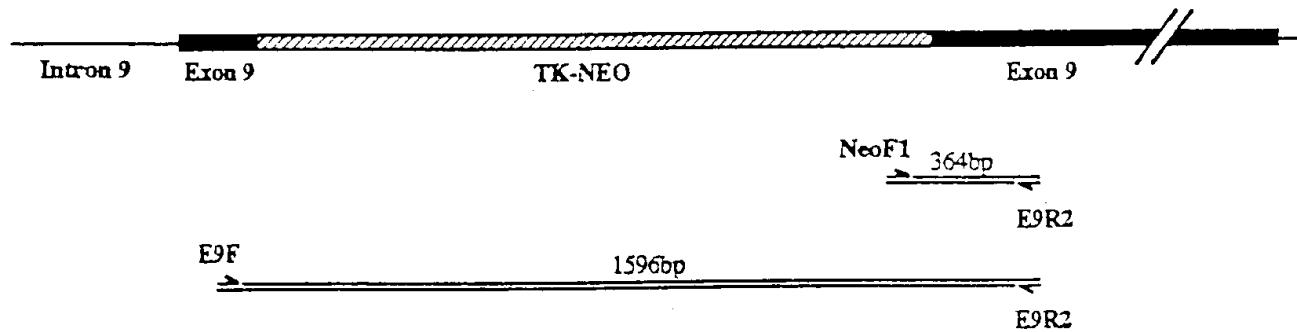


Fig. 22

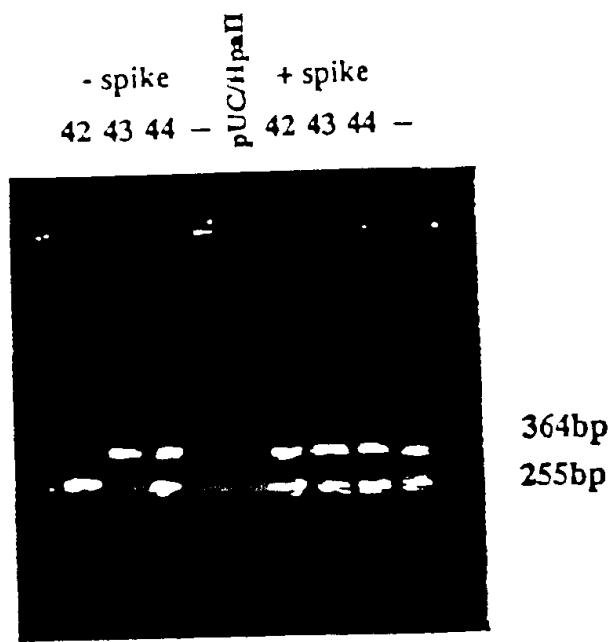
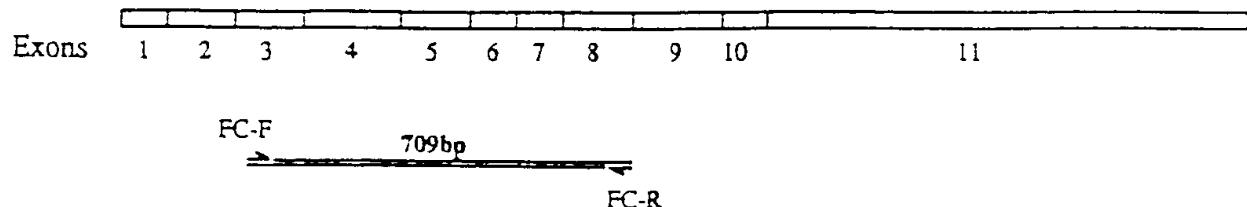
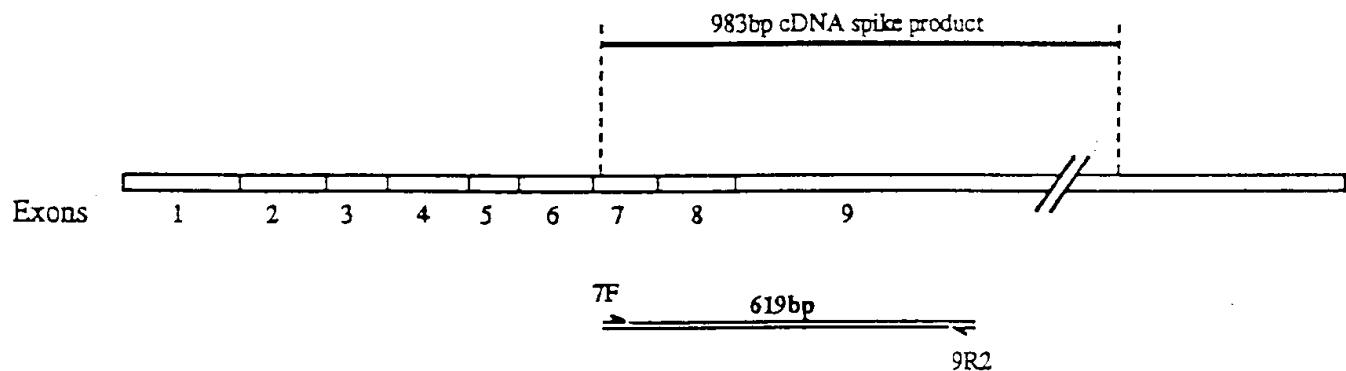


Fig. 23

Primer binding sites within mouse ferrochelatase cDNA



Primer binding sites within mouse  $\alpha$ -1,3-GalT cDNA



## i) Ferrochelatase, FC-F/R

M, Marker SPP-I  
 C, MQW control  
 K, KIDNEY  
 H, HEART  
 L, LIVER

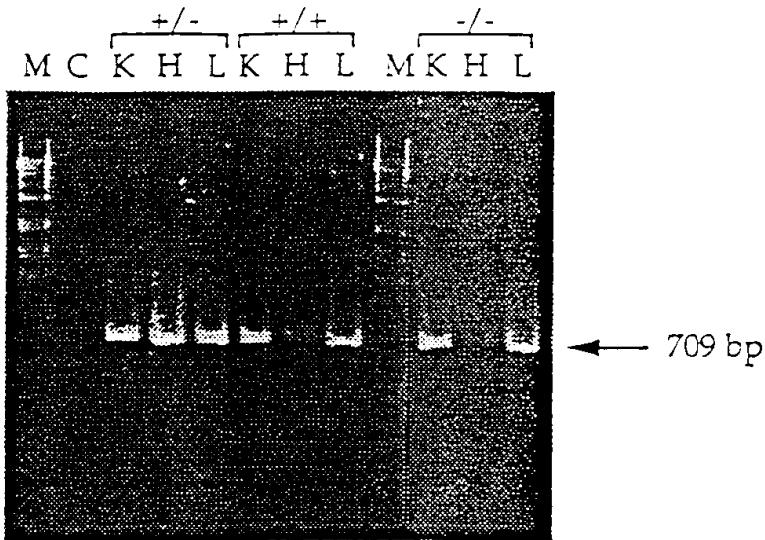
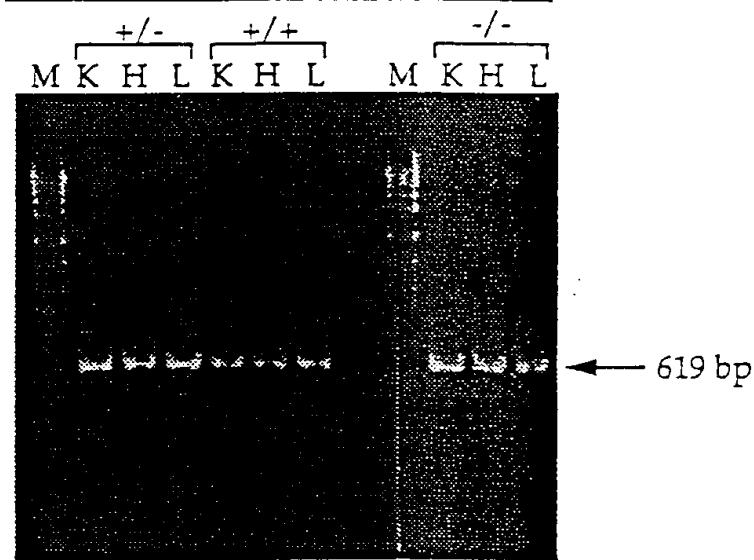
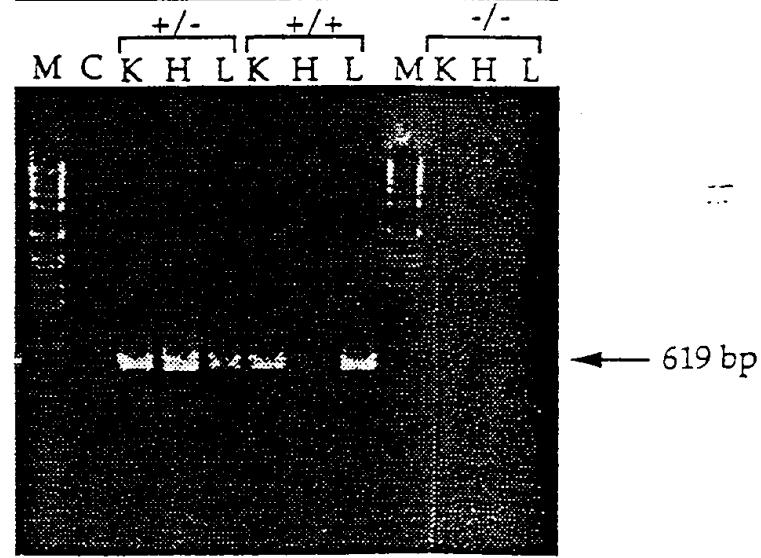
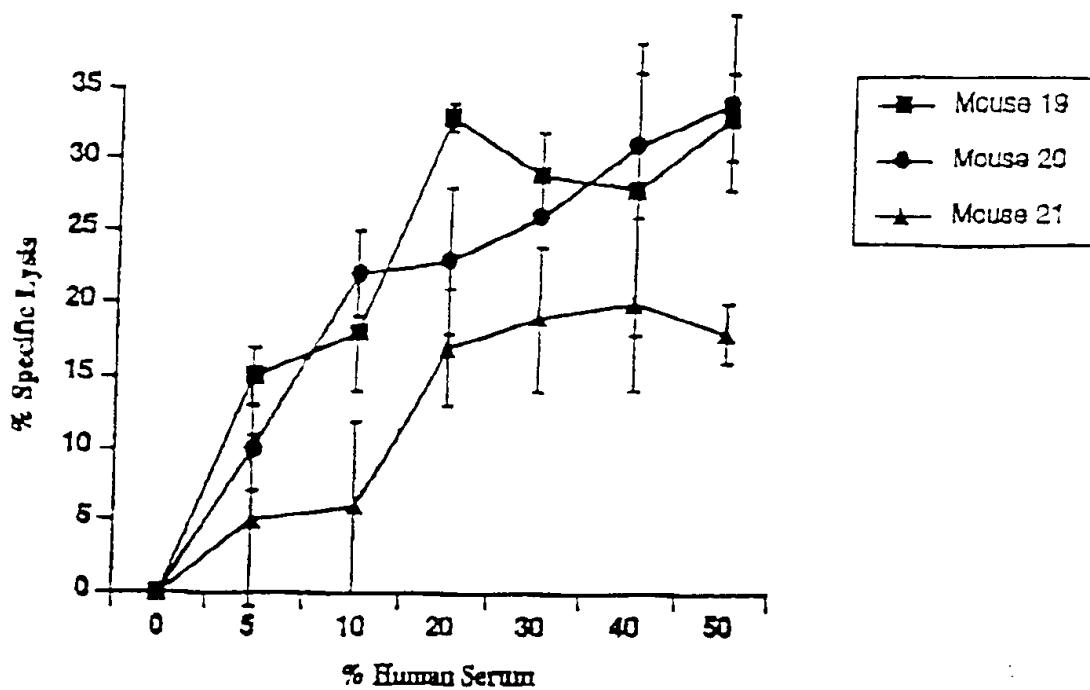
ii)  $\alpha$ -1,3-GT cDNA spike  
+ 7F/9R2 primersiii)  $\alpha$ -1,3-GT 7F/9R2 primers

Fig. 25



Mouse 19: Wild type; Mouse 20: Heterozygote Gal KO; Mouse 21: Homozygous Gal KO

Fig. 26

T-LIF SEQUENCE - Murine

CTGACACCTTCGCTTCCTCTGGCTCTCCGCTGGACCTTCCCCACCCC  
GGCCTCTTCCTGGTGCACCACTCCCTTCATTCAAAGGATTGTGCCCTTA  
CTGCTGCTGGTCTGCACTGGAAACACGGGGAGGGAGCCCTTTCCCATCAC  
CCCTGTAAAATGCCACCTGTGCCATGCCACCCATGCCACGGCAACCTC  
Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly  
ATG AAC CAG ATC AAG AAT CAA CTG GCA CAG CTC AAT GGC  
Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly  
AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA GCT CAA GGX  
Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro Asn  
GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT AAC  
Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys  
ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG  
Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser  
ACC AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC  
Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn  
GCC TCC CTG ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC  
Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile  
CCC ACT GCC GTG AGC CTC CAG GTC AAG CTC AAT GCT ACT ATA  
Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu  
GAC GTC ATG AGG GGC CTC AGC AAT GTG CTT TGC CGT CTG  
Cys Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val  
TGC AAC AAG TAC CGT GTG GGC CAC GTG GAT GTG CCA CCT GTC  
Phe Asp His Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu  
CCC GAC TCT GAC AAA GAA GCC TTC CAA AGG AAA AAG TTG  
Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser Val  
GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT GTG  
Val Val Gln Ala Phe \*\*\*  
GTG GTC CAG GCC TTC TAG AGAGGAGGTCTGAATGTACCATGGACTG...

Fig. 27

HUMAN T-LIF SEQUENCE

GACCTTTGC	CTTTTCTCTC	TCCTGGTGCA	CCATTTCTC	TCCCTCCCTG	50
AGCCGGAGTT	GTGCCCCCTGC	TGTTGGTTCT	GCACTGGAAA	CATGGGGCGG	100
GGAGCCCCCT	CCCCATCACC	CCTGTCAACG	CCACCTGTGC	CATA CGCCAC	150
CCATGTCACA	ACAAACCTC	ATG AAC CAG ATC			182
Met Asn Gln Ile					
AGG AGC CAA CTG GCA	CAG CTC AAT GGC	AGT GCC AAT GCC	CTC		227
Arg Ser Gln Leu Ala	Gln Leu Asn Gly	Ser Ala Asn Ala	Leu		
5	10	15			
TTT ATT CTC TAT TAC ACA	GCC CAG GGG GAG CCG	TTC CCC AAC			272
Phe Ile Leu Tyr Tyr	Thr Ala Gln Gly	Glu Pro Phe Pro	Asn		
20	25	30			
AAC CTG GAC AAG CTA	TGT GGC CCC AAC	GTG ACG GAC TTC	CCG		317
Asn Leu Asp Lys Leu	Cys Gly Pro Asn Val	Thr Asp Phe Pro			
35	40	45			
CCC TTC CAC GCC AAC	GGC ACG GAG AAG	GCC AAG CTG GTG GAG			362
Pro Phe His Ala Asn	Gly Thr Glu Lys Ala	Lys Leu Val Glu			
50	55	60			
CTG TAC CGC ATA GTC	GTG TAC CTT GGC ACC	TCC CTG GGC AAC			407
Leu Tyr Arg Ile Val	Val Tyr Leu Gly	Thr Ser Leu Gly Asn			
65	70				
ATC ACC CGG GAC CAG	AAG ATC CTC AAC CCC	AGT GCC CTC AGC			452
Ile Thr Arg Asp Gln	Lys Ile Leu Asn Pro	Ser Ala Leu Ser			
75	80	85			
CTC CAC AGC AAG CTC AAC	GCC ACC GAC ATC	CTG CGA GGC			497
Leu His Ser Lys Leu	Asn Ala Thr Ala Asp	Ile Leu Arg Gly			
90	95	100			
CTC CTT AGC AAC GTG	CTG TGC CGC CTG TGC	AGC AAG TAC CAC			542
Leu Leu Ser Asn Val	Leu Cys Arg Leu Cys	Ser Lys Tyr His			
105	110	115			
GTG GGC CAT GTG GAC	GTG ACC TAC GGC CCT	GAC ACC TCG GGT			587
Val Gly His Val Asp	Val Thr Tyr Gly	Pro Asp Thr Ser Gly			
120	125	130			
AAG GAT GTC TTC CAG	AAG AAG CTG GGC TGT	CAA CTC CTG			632
Lys Asp Val Phe Gln	Lys Lys Lys Leu	Gly Cys Gln Leu			

Fig. 27 (cont.)

27-2

135	140	
GGG AAG TAT AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC		677
Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe		
145	150	155
TAG CAGGAGGTCT		722

\*\*\*

Fig. 28

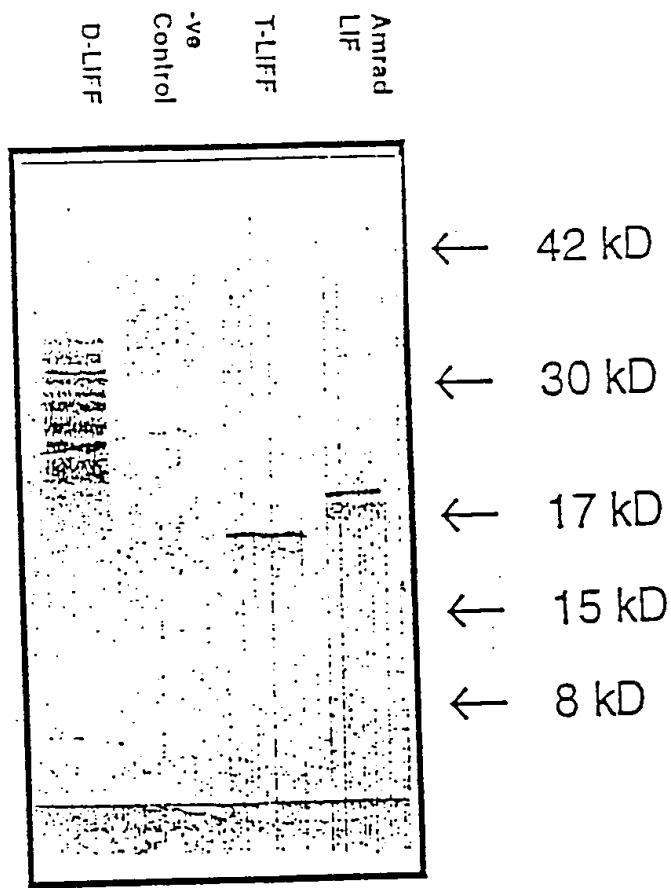
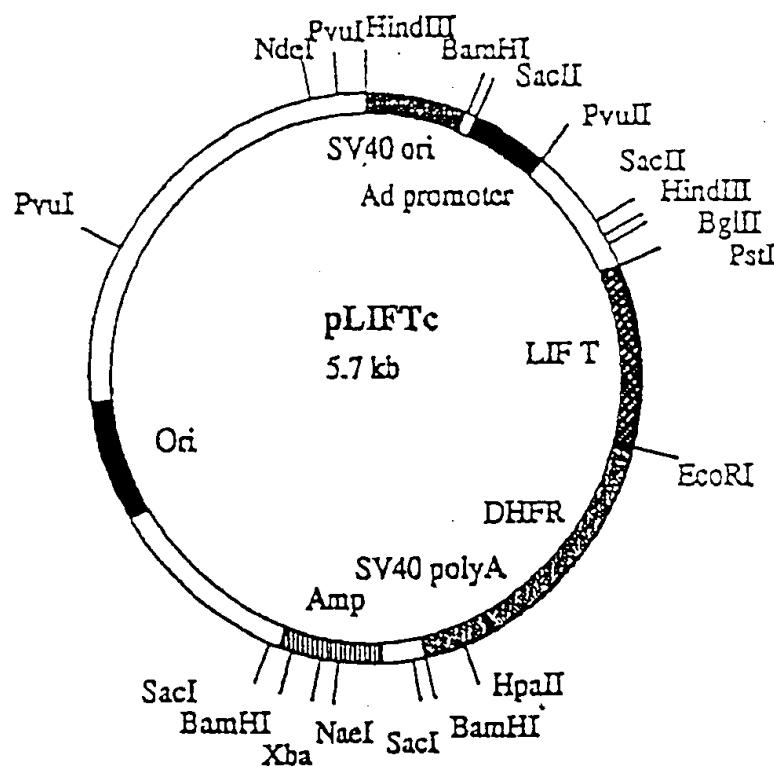


Fig. 29

(3c)



- SV40 origin of replication
- Adenovirus promoter
- LIF T coding region
- Dihydrofolate reductase 3' end
- Ampicillin resistance gene
- Bacterial origin of replication

Fig. 30

